

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2006, 07:43:54 ; Search time 38 Seconds
(without alignments)
238.010 Million cell updates/sec

Title: US-09-688-566-81

Perfect score: 494

Sequence: 1 VSDPRDLVVAAPTSLRI.....VTDKSDTKYDDPISINVRT 94

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	361	73.1	2386	1 FNHU	fibronectin precu
2	354	71.7	2265	1 FNBO	fibronectin - bovi
3	333	67.4	2477	2 S14428	fibronectin - precu
4	311	63.0	273	2 A28512	fibronectin - chic
5	311	63.0	1020	2 A29355	fibronectin - chic
6	262	53.0	2481	2 A43908	fibronectin - Afri
7	125	25.3	4006	2 T09070	probable tenascin
8	124	25.1	4135	2 T42629	tenascin-X - bovin
9	121	24.5	1353	1 JH0675	restricatin precurs
10	121	24.5	1746	1 S19694	tenascin precursor
11	116	23.5	1356	2 A45445	janusin precursor,
12	111	22.5	3566	1 A40701	tenascin-X precurs
13	110.5	22.4	1898	2 S46216	leukocyte antigen-
14	110	22.3	2019	1 JQ1322	tenascin precursor
15	108	21.9	933	2 A31930	cytotactin - chick
16	108	21.9	1810	1 A32230	tenascin precursor
17	106.5	21.6	2944	2 A54849	collagen alpha 1(V
18	105	21.3	2201	2 A32160	tenascin-X - human
19	102	20.6	417	2 S65178	tenascin-X - pig (
20	100	20.2	1912	2 A56178	protein-tyrosine-p
21	98.5	19.9	647	2 A43902	tenascin - eastern
22	96	19.4	1290	2 A56493	leucocyte common a
23	96	19.4	3124	2 A40020	collagen alpha 1(X
24	94	19.0	843	2 A40970	undulin 1 - human
25	92	18.6	1691	1 D54689	protein-tyrosine-p
26	92	18.6	1894	2 C54689	protein-tyrosine-p
27	91.5	18.5	147	2 S00848	fibronectin, trans
28	90.5	18.3	440	2 I50213	protein-tyrosine-p
29	88.5	17.9	189	2 S71465	fibronectin - chic

ALIGNMENTS

RESULT 1

FNHU

fibronectin precursor [validated] - human

N;Alternate names: fibronectin splice form ED-A

C;Species: Homo sapiens (man)

C;Date: 27-Nov-1985 #sequence revision 31-Mar-1993 #text change 31-Dec-2004

C;Accession: A26460; A26284; S03917; A24854; A24476; A91008; A93529; A21011; A90495; A22

R;Dean, D.C.; Bowlin, C.L.; Bourgeois, S.

Proc. Natl. Acad. Sci. U.S.A. 84, 1876-1880, 1987

A;Title: Cloning and analysis of the promoter region of the human fibronectin gene.

A;Reference number: A26460; MUID:87175578; PMID:3031656

A;Accession: A26460

A;Molecule type: DNA

A;Residues: 1-49 <DEA>

A;Cross-references: UNIPROT:P02751; UNIPROT:Q14327; UNIPARC:UPI000016A926; GB:M15801; NI

R;Oldberg, A.; Ruoslahti, E.

J. Biol. Chem. 261, 2113-2116, 1986

A;Title: Evolution of the fibronectin gene.

A;Reference number: A26284; MUID:86111901; PMID:3003095

A;Accession: A26284

A;Molecule type: DNA

A;Residues: 1447-1540 <OLD>

A;Cross-references: UNIPARC:UPI0000112E37; GB:M12549; NID:g182688

A;Note: the authors translated the codon TTC for residue 1494 as Glu

R;Paolella, G.; Henschcliff, C.; Sebastio, G.; Baralle, F.E.

Nucleic Acids Res. 16, 3545-3557, 1988

A;Title: Sequence analysis and in vivo expression show that alternative splicing of ED-B

A;Reference number: S00848; MUID:88233940; PMID:3375063

A;Accession: S03917

A;Molecule type: DNA

A;Residues: 1594-1767, 'V', 1769-1783 <PAO>

A;Cross-references: UNIPARC:UPI000017432B; EMBL:X07718; NID:g31402

A;Note: the authors translated the codon AAC for residue 1631 as Asp

R;Vibe-Pedersen, K.; Magnusson, S.; Baralle, F.E.

FEBS Lett. 207, 287-291, 1986

A;Title: Donor and acceptor splice signals within an exon of the human fibronectin gene:

A;Reference number: A24854; MUID:87030929; PMID:3770201

A;Accession: A24854

A;Molecule type: DNA

A;Residues: 1992-2147 <VIB>

A;Cross-references: UNIPARC:UPI000017432C; GB:X04530; NID:g31436

R;Gutman, A.; Yanada, K.M.; Kornblihtt, A.

FEBS Lett. 207, 145-148, 1986

A;Title: Human fibronectin is synthesized as a pre-propolypeptide.

A;Reference number: A24476; MUID:87030890; PMID:3770189

A;Accession: A24476

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-14, 'Q', 16-38 <GUT>

A;Cross-references: UNIPARC:UPI000017432D

R;Kornblihtt, A.R.; Umezawa, K.; Vibe-Pedersen, K.; Baralle, F.E.

EMBO J. 4, 1755-1759, 1985

tenascin - rat (fr
fibronectin ED-B -
leukocyte antigen-
protein-tyrosine-p
tenascin-X - mouse
fibronectin ED-A -
nephlin - human
type XII collagen
collagen alpha 1(X
collagen alpha 1(X
collagen alpha 1(X
tenascin Y precurs
protein-tyrosine-p
protein-tyrosine-p
undulin 2 - human
hypothetical prote

30 88.5 17.9 575 2 A54861
31 87.5 17.7 90 2 I46162
32 87 17.6 1897 1 TDHULK
33 86 17.4 1711 1 A55148
34 83 16.8 860 2 I48839
35 82 16.6 89 2 I46161
36 82 16.6 1241 2 T37190
37 81.5 16.5 929 2 I51027
38 81.5 16.5 1747 2 A45974
39 81.5 16.5 1857 2 S31212
40 81.5 16.5 1888 2 S78476
41 80 16.2 1914 2 T42635
42 79 16.0 2029 1 TDFPLK
43 78 15.8 1337 1 I38670
44 77.5 15.7 445 2 B40970
45 77 15.6 725 2 A90255

A;Title: Primary structure of human fibronectin: differential splicing may generate at l
A;Reference number: A91008; MUID:85284965; PMID:2992939
A;Accession: A91008
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 32-1344, 1346-2080, 2112-2386 <KOR>
A;Cross-references: UNIPARC:UPI000017432E; UNIPARC:UPI000017433F; GB:X02761
R;Kornblitt, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Nucleic Acids Res. 12, 5853-5868, 1984
A;Title: Human fibronectin: cell specific alternative mRNA splicing generates polypeptid
A;Reference number: A93529; MUID:84272258; PMID:6462919
A;Accession: A93529
A;Molecule type: mRNA
A;Residues: 973-2080, 2112-2386 <X02>
A;Cross-references: UNIPARC:UPI000017432F; UNIPARC:UPI0000174330; GB:X00739
R;Oldberg, A.; Linney, E.; Ruoslahti, E.
J. Biol. Chem. 258, 10193-10196, 1983
A;Title: Molecular cloning and nucleotide sequence of a cDNA clone coding for the cell a
A;Reference number: A21011; MUID:83230929; PMID:6888418
A;Accession: A21011
A;Molecule type: mRNA
A;Residues: 1434-1537 <OL2>
A;Cross-references: UNIPARC:UPI0000174331; GB:X00055; NID:g182680; PIDN:AAAS2459.1; PID:
R;Bernard, M.P.; Kolbe, M.; Weil, D.; Chu, M.L.
Biochemistry 24, 2698-2704, 1985
A;Title: Human cellular fibronectin: comparison of the carboxyl-terminal portion with ra
A;Reference number: A90495; MUID:85280409; PMID:2992573
A;Accession: A90495
A;Molecule type: mRNA
A;Residues: 1594-2386 <BER>
A;Cross-references: UNIPARC:UPI000016A928; GB:M10905; NID:g182696; PIDN:AAAS2462.1; PID:
R;Umezawa, K.; Kornblitt, A.R.; Baralle, F.E.
FEBS Lett. 186, 31-34, 1985
A;Title: Isolation and characterization of cDNA clones for human liver fibronectin.
A;Reference number: A22245; MUID:85231203; PMID:2989004
A;Accession: A22245
A;Molecule type: mRNA
A;Residues: 1948-2067 <UME>
A;Cross-references: UNIPARC:UPI000000046A; GB:M27589; NID:g182705; PIDN:AAAS2465.1; PID:
A;Accession: B22245
A;Molecule type: mRNA
A;Residues: 1975-1991, 2017-2039 <UM2>
A;Cross-references: UNIPARC:UPI0000174332; UNIPARC:UPI0000174333; GB:M27590
R;Sekiguchi, K.; Kioe, A.M.; Kurachi, K.; Yoshitake, S.; Hakomori, S.
Biochemistry 25, 4936-4941, 1986
A;Title: Human liver fibronectin complementary DNAs: identification of two different mes
A;Reference number: I52394; MUID:87026578; PMID:3021206
A;Accession: I65273
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1978-1990, 2016-2018, 'N', 2020-2081, 2113-2127 <SEK>
A;Cross-references: UNIPARC:UPI000006E04C; GB:M14060; NID:g182701; PIDN:AAAS2464.1; PID:
R;Kornblitt, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983
A;Title: Isolation and characterization of cDNA clones for human and bovine fibronectin
A;Reference number: A21165; MUID:83221567; PMID:6304699
A;Accession: A21165
A;Molecule type: mRNA
A;Residues: 2291-2386 <K03>
A;Cross-references: UNIPARC:UPI0000174334; GB:X00799; NID:g182681; PIDN:AAAS2460.1; PID:
R;Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
J. Biol. Chem. 258, 12670-12674, 1983
A;Title: Primary structure of human plasma fibronectin.
A;Reference number: A92398; MUID:84032463; PMID:6630202
A;Accession: A92398
A;Molecule type: protein
A;Residues: 32-47, 'C', 49-51, 'S', 53-72, 'A', 74-290 <GAR>
A;Cross-references: UNIPARC:UPI0000174335
R;Garcia-Pardo, A.; Gold, L.I.
Arch. Biochem. Biophys. 304, 181-188, 1993
A;Title: Further characterization of the binding of fibronectin to gelatin reveals the p
A;Reference number: S34791; MUID:93312001; PMID:8323285
A;Accession: S34791
A;Molecule type: protein
A;Residues: 291-300, 551-560 <GAR2>
A;Cross-references: UNIPARC:UPI0000174336; UNIPARC:UPI0000174337
R;Griffin, C.A.; Calaycay, J.; Shively, J.E.; Smith, R.L.
Thromb. Res. 43, 469-477, 1986
A;Title: Two plasma fibronectin fragments with different gelatin-binding properties.
A;Reference number: A60904; MUID:87019725; PMID:3532418
A;Accession: A60904
A;Molecule type: protein
A;Residues: 293-301 <GRI>
A;Cross-references: UNIPARC:UPI0000174338
R;Calaycay, J.; Pande, H.; Lee, T.; Borsi, L.; Siri, A.; Shively, J.E.; Zardi, L.
J. Biol. Chem. 260, 12136-12141, 1985
A;Title: Primary structure of a DNA- and heparin-binding domain (domain III) in human pla
A;Reference number: A23901; MUID:86008277; PMID:3900070
A;Accession: A23901
A;Molecule type: protein
A;Residues: 616-677, 'Q', 679-703, 'PT', <CAL>
A;Cross-references: UNIPARC:UPI0000174339
R;Pierschbacher, M.D.; Ruoslahti, E.; Sundelin, J.; Lind, P.; Peterson, P.A.
J. Biol. Chem. 257, 9593-9597, 1982
A;Title: The cell attachment domain of fibronectin. Determination of the primary structu
A;Reference number: A92386; MUID:82265604; PMID:7050098
A;Accession: A92386
A;Molecule type: protein
A;Residues: 1441-1548 <PIE>
A;Cross-references: UNIPARC:UPI0000141CD5
A;Note: residues 1524-1527 are responsible for the cell-binding activity
R;Garcia-Pardo, A.; Rostagno, A.; Frangione, B.
Biochem. J. 241, 923-928, 1987
A;Title: Primary structure of human plasma fibronectin. Characterization of a 38 kDa dom
A;Reference number: A32517; MUID:87241275; PMID:3593230
A;Accession: A32517
A;Molecule type: protein
A;Residues: 1589-1630, 'T', 1722-2058 <GAR3>
A;Cross-references: UNIPARC:UPI000017433A
R;Fressel, T.; McCarthy, J.B.; Calaycay, J.; Lee, T.D.; Legesse, K.; Shively, J.E.; Pand
Biochem. J. 274, 731-738, 1991
A;Title: Human plasma fibronectin. Demonstration of structural differences between the A-
A;Reference number: S14357; MUID:91190085; PMID:2012601
A;Accession: S14357
A;Molecule type: protein
A;Residues: 1614-1630, 'T', 1722-2081, 2113-2244 <TRE>
A;Cross-references: UNIPARC:UPI000017433B
R;Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.
J. Biol. Chem. 260, 10320-10325, 1985
A;Title: Primary structure of human plasma fibronectin. Characterization of a 31,000-dalt
A;Reference number: A23891; MUID:85261459; PMID:4019516
A;Accession: A23891
A;Molecule type: protein
A;Residues: 2071-2080, 2112-2356 <GAR4>
A;Cross-references: UNIPARC:UPI000017433C; UNIPARC:UPI000017433D
C;Comment: The extra domain and connecting strand 3 are subject to developmental and tiss
C;Comment: The cellular and plasma fibronectins are high molecular weight glycoproteins,
ation, and transformation.
C;Genetics:
A;Gene: GDB:FNI
A;Cross-references: GDB:119135; OMIM:135600
A;Map position: 2q34-q34
A;Introns: 49/3; 1266/1; 1357/1; 1447/1; 1487/1; 1541/1; 1631/1; 1721/1; 1991/1; 2145/1
C;Superfamily: fibronectin type I repeat homology; fibronectin type II repeat homology; f
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-31/Domain: propeptide #status predicted <PRO>
F;32-2386/Product: fibronectin #status experimental
F;52-272/Domain: fibrin and heparin binding <PHB>
F;52-87/Domain: fibronectin type I repeat homology <PHB>
F;97-135/Domain: fibronectin type I repeat homology <IF1>
F;141-179/Domain: fibronectin type I repeat homology <IF2>
F;186-225/Domain: fibronectin type I repeat homology <IF3>
F;231-270/Domain: fibronectin type I repeat homology <IF4>
F;308-608/Domain: collagen binding <CBR>
F;308-342/Domain: fibronectin type I repeat homology <IF6>

F;360-401/Domain: fibronectin type II repeat homology <2F1>
F;420-461/Domain: fibronectin type II repeat homology <2F2>
F;470-508/Domain: fibronectin type I repeat homology <1F7>
F;518-555/Domain: fibronectin type I repeat homology <1F8>
F;561-599/Domain: fibronectin type I repeat homology <1F9>

Query Match 73.1%; Score 361; DB 1; Length 2386;
Best Local Similarity 77.7%; Pred. No. 1.8e-28;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLVVAATPTSLRLISWNRSGLQSYRYITYTGTCGNSPVQSFVPPWASIIATIS 60
DB 1447 VSDVPRDLVVAATPTSLRLISWNRSGLQSYRYITYTGTCGNSPVQSFVPPWASIIATIS 1506
QY 61 GLKPGVDYTTIVAVTDKSTPKYDDPISINVRT 94
DB 1507 GLKPGVDYTTIVAVTGRGDSPASSKPFISINVRT 1540

RESULT 2
FNBO
fibronectin - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1988 #sequence revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A26452; B21165; A23292
R;Skorstengaard, K.; Jensen, M.S.; Sahl, P.; Petersen, T.E.; Magnusson, S.
Eur. J. Biochem. 161, 441-453, 1986
A;Title: Complete primary structure of bovine plasma fibronectin.
A;Reference number: A26452; MUID:87054047; PMID:3780752
A;Accession: A26452
A;Molecule type: protein
A;Residues: 1-2265 <SKO>
A;Cross-references: UNIPROT:P07589; UNIPARC:UPI000012A7BE
R;Kornblitt, A.R.; Vibe-Pedersen, K.; Baralle, F.E.
Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983
A;Title: Isolation and characterization of cDNA clones for human and bovine fibronectin
A;Reference number: A21165; MUID:83221567; PMID:6304699
A;Accession: B21165
A;Molecule type: mRNA
A;Residues: 2170-2265 <KOR>
A;Cross-references: UNIPARC:UPI000016C30C; GB:K00800; NID:g163055; PIDN:AAA30521.2; PID:
R;Petersen, T.E.; Thøgersen, H.C.; Skorstengaard, K.; Vibe-Pedersen, K.; Sahl, P.; Sottr
Proc. Natl. Acad. Sci. U.S.A. 80, 137-141, 1983
A;Title: Partial primary structure of bovine plasma fibronectin: three types of internal
A;Reference number: A23292; MUID:83117805; PMID:6218503
A;Accession: A23292
A;Molecule type: protein
A;Residues: 1-16,'C',18-20,'S',22-432;447-463;1367-1517;1567-1673;2062-2176,'N',2178-226
A;Cross-references: UNIPARC:UPI0000174338; UNIPARC:UPI000017433F; UNIPARC:UPI0000174340;
C;Comment: Cys-1201 and Cys-2015 have free sulfhydryl groups.
C;Comment: The plasma fibronectin molecule consists of two chains, which are connected b
C;Comment: Fibronectins bind cell surfaces and various compounds including collagen, fib
aling, and maintenance of cell shape.
C;Comment: Plasma fibronectin is synthesized by hepatocytes.
C;Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repe
C;Keywords: acute phase; alternative splicing; collagen binding; duplication; extracellu
F;21-241/Domain: fibrin and heparin binding <FBR>
F;21-56/Domain: fibronectin type I repeat homology <1F1>
F;66-104/Domain: fibronectin type I repeat homology <1F2>
F;110-148/Domain: fibronectin type I repeat homology <1F3>
F;155-194/Domain: fibronectin type I repeat homology <1F4>
F;200-239/Domain: fibronectin type I repeat homology <1F5>
F;277-577/Domain: collagen binding <CBR>
F;277-311/Domain: fibronectin type I repeat homology <1F6>
F;329-370/Domain: fibronectin type II repeat homology <2F1>
F;389-430/Domain: fibronectin type II repeat homology <2F2>
F;439-477/Domain: fibronectin type I repeat homology <1F7>
F;487-524/Domain: fibronectin type I repeat homology <1F8>
F;530-568/Domain: fibronectin type I repeat homology <1F9>
F;578-661/Domain: fibronectin type III repeat homology <FN3A>
F;688-770/Domain: fibronectin type III repeat homology <FN3B>
F;779-860/Domain: fibronectin type III repeat homology <FN3C>
F;875-957/Domain: fibronectin type III repeat homology <FN3D>

F;965-1046/Domain: fibronectin type III repeat homology <FN3E>
F;1055-1134/Domain: fibronectin type III repeat homology <FN3F>
F;1142-1227/Domain: fibronectin type III repeat homology <FN3G>
F;1235-1318/Domain: fibronectin type III repeat homology <FN3H>
F;1326-1404/Domain: fibronectin type III repeat homology <GN3I>
F;1410-1517/Domain: cell attachment <CAD>
F;1416-1502/Domain: fibronectin type III repeat homology <FN3J>
F;1493-1495/Region: cell attachment (R-G-D) motif
F;1510-1592/Domain: fibronectin type III repeat homology <FN3K>
F;1600-1870/Domain: heparin binding <HB2>
F;1600-1682/Domain: fibronectin type III repeat homology <FN3L>
F;1692-1773/Domain: fibronectin type III repeat homology <FN3M>
F;1781-1863/Domain: fibronectin type III repeat homology <FN3N>
F;1970-1972/Region: cell attachment (R-G-D) motif
F;1982-2062/Domain: fibronectin type III repeat homology <FN3O>
F;1985-2216/Domain: fibrin binding <FB2>
F;2085-2124/Domain: fibronectin type I repeat homology <1F10>
F;2130-2167/Domain: fibronectin type I repeat homology <1F11>
F;2174-2209/Domain: fibronectin type I repeat homology <1F12>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;2/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of fibrin) #status experime
F;21-47,45-56,66-94,92-104,110-138,136-148,155-184,182-194,200-229,227-239,277-304,302-3
7,2155-2167,2174-2200,2198-2209/Disulfide bonds: #status predicted
F;1205,1692/Binding site: carbohydate (Asn) (covalent) #status absent
F;1943,1944/Binding site: carbohydate (Thr) (covalent) #status experimental
F;2246/Disulfide bonds: interchain (to 2250) #status predicted
F;2250/Disulfide bonds: interchain (to 2246) #status predicted
F;2263/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 71.7%; Score 354; DB 1; Length 2265;
Best Local Similarity 74.5%; Pred. No. 8.8e-28;
Matches 70; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLVVAATPTSLRLISWNRSGLQSYRYITYTGTCGNSPVQSFVPPWASIIATIS 60
DB 1416 VSDVPRDLVVAATPTSLRLISWNRSGLQSYRYITYTGTCGNSPVQSFVPPWASIIATIS 1475
QY 61 GLKPGVDYTTIVAVTDKSTPKYDDPISINVRT 94
DB 1476 GLKPGVDYTTIVAVTGRGDSPASSKPFVSINVRT 1509

RESULT 3
S14428
fibronectin precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1994 #sequence revision 28-Oct-1994 #text change 09-Jul-2004
C;Accession: S14428; S12455; A22319; S46203; S00459; A27252; I59049
R;Hynes, R.O.
submitted to the EMBL Data Library, July 1989
A;Reference number: S14428
A;Accession: S14428
A;Molecule type: mRNA
A;Residues: 1-2477 <HYN>
A;Cross-references: UNIPROT:P04937; UNIPARC:UPI000012A7C6; EMBL:X15906; NID:g56163; PIDN:
R;Schwarzbauer, J.E.; Patel, R.S.; Fonda, D.; Hynes, R.O.
EMBO J. 6, 2573-2580, 1987
A;Title: Multiple sites of alternative splicing of the rat fibronectin gene transcript.
A;Reference number: S12455; MUID:88054951; PMID:2445560
A;Accession: S12455
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 609-1810,'T',1812-2283 <SCH>
A;Cross-references: UNIPARC:UPI0000177AEA; EMBL:X15906
R;Tamkun, J.W.; Schwarzbauer, J.E.; Hynes, R.O.
Proc. Natl. Acad. Sci. U.S.A. 81, 5140-5144, 1984
A;Title: A single rat fibronectin gene generates three different mRNAs by alternative sp
A;Reference number: A22319; MUID:84238097; PMID:6089177
A;Accession: A22319
A;Molecule type: DNA
A;Residues: 2052-2237 <TAM>
A;Cross-references: UNIPARC:UPI0000177AEB

R;Falkenberg, C.; Enghild, J.J.; Thøgersen, I.B.; Salvesen, G.; Akerstroem, B.
Biochem. J. 301, 745-751, 1994
A;Title: Isolation and characterization of fibronectin-alpha(1)-microglobulin complex in
A;Reference number: S46203; MUID:94330948; PMID:7519849
A;Accession: S46203
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1183-1192; GLN', 1268, 'P', 1270-1271, 'D', 1273, 'CF', 1276, 'PY', 1385-1399 <FAL>
A;Cross-references: UNIPARC:UPI0000177AEC; UNIPARC:UPI0000177AED; UNIPARC:UPI0000177AEE
R;Patel, R.S.; Oedermarkt, E.; Schwarzbauer, J.E.; Hynes, R.O.
EMBO J. 6, 2565-2572, 1987
A;Title: Organization of the fibronectin gene provides evidence for exon shuffling during
A;Reference number: S00459; MUID:88054950; PMID:3119323
A;Accession: S00459
A;Molecule type: DNA
A;Residues: 1-139; 2382-2477 <PAT>
A;Cross-references: UNIPARC:UPI000017095C; UNIPARC:UPI0000177AER; EMBL:X05831
A;Note: the authors translated the codon CCT for residues 51 and 94 as Ala
R;Schwarzbauer, J.E.; Tamkun, J.W.; Lemischka, I.R.; Hynes, R.O.
Cell 35, 421-431, 1983
A;Title: Three different fibronectin mRNAs arise by alternative splicing within the coding
A;Reference number: A27252; MUID:84082067; PMID:6317187
A;Accession: A27252
A;Molecule type: mRNA
A;Residues: 1586-1720, 'T', 1722, 1813-2477 <SC2>
A;Cross-references: UNIPARC:UPI0000177AF0
R;Oedermarkt, E.; Tamkun, J.W.; Hynes, R.O.
Proc. Natl. Acad. Sci. U.S.A. 82, 6571-6575, 1985
A;Title: Repeating modular structure of the fibronectin gene: Relationship to protein structure
A;Reference number: I59049; MUID:86016741; PMID:3863113
A;Accession: I59049
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1722-1810 <RES>
A;Cross-references: UNIPARC:UPI000000040C; GB:M11750; NID:G204164; PIDN:AAA41170.1; PID:
C;Genetics:
A;Introns: 51/1; 94/1; 2416/3; 2454/3
C;Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat
C;Keywords: alternative splicing; cell adhesion; collagen binding; disulfide bond; duplication
F;1-32/Domain: signal sequence #status predicted <SIG>
F;232-271/Domain: fibronectin type I repeat homology <1F5>
F;33-2477/Product: fibronectin #status predicted <MAT>
F;53-88/Domain: fibronectin type I repeat homology <1F1>
F;98-136/Domain: fibronectin type I repeat homology <1F2>
F;142-180/Domain: fibronectin type I repeat homology <1F3>
F;187-226/Domain: fibronectin type I repeat homology <1F4>
F;232-271/Domain: fibronectin type I repeat homology <1F5>
F;308-342/Domain: fibronectin type I repeat homology <1F6>
F;360-401/Domain: fibronectin type II repeat homology <2F1>
F;420-461/Domain: fibronectin type II repeat homology <2F2>
F;470-508/Domain: fibronectin type I repeat homology <1F7>
F;518-555/Domain: fibronectin type I repeat homology <1F8>
F;561-599/Domain: fibronectin type I repeat homology <1F9>
F;609-692/Domain: fibronectin type III repeat homology <FN3A>
F;718-800/Domain: fibronectin type III repeat homology <FN3B>
F;809-890/Domain: fibronectin type III repeat homology <FN3C>
F;905-987/Domain: fibronectin type III repeat homology <FN3D>
F;995-1076/Domain: fibronectin type III repeat homology <FN3E>
F;1085-1164/Domain: fibronectin type III repeat homology <FN3F>
F;1172-1257/Domain: fibronectin type III repeat homology <FN3G>
F;1265-1348/Domain: fibronectin type III repeat homology <FN3H>
F;1356-1439/Domain: fibronectin type III repeat homology <FN3I>
F;1447-1529/Domain: fibronectin type III repeat homology <FN3J>
F;1537-1619/Domain: fibronectin type III repeat homology <FN3K>
F;1614-1616/Region: cell attachment (R-G-D) motif
F;1631-1713/Domain: fibronectin type III repeat homology <FN3L>
F;1721-1803/Domain: fibronectin type III repeat homology <FN3M>
F;1811-1893/Domain: fibronectin type III repeat homology <FN3N>
F;1903-1984/Domain: fibronectin type III repeat homology <FN3O>
F;1992-2074/Domain: fibronectin type III repeat homology <FN3P>
F;2181-2183/Region: cell attachment (R-G-D) motif
F;2193-2273/Region: fibronectin type III repeat homology <FN3Q>
F;2296-2335/Domain: fibronectin type I repeat homology <1F10>
F;2341-2378/Domain: fibronectin type I repeat homology <1F11>

F;2385-2420/Domain: fibronectin type I repeat homology <1F12>
F;53-79, 77-88, 98-126, 124-136, 142-170, 168-180, 187-216, 214-226, 232-261, 259-271, 308-335, 333
368, 2366-2378, 2385-2411, 2409-2420/Disulfide bonds: #status predicted
F;2458/Disulfide bonds: interchain (to 2462) #status predicted
F;2462/Disulfide bonds: interchain (to 2458) #status predicted
Query Match 67.4%; Score 333; DB 2; Length 2477;
Best Local Similarity 68.1%; Pred. No. 1.4e-25;
Matches 64; Conservative 10; Mismatches 20; Indels 0; Gaps 0;
QY 1 VSDVPRDLVVAATPTSLRISWNRSGLQSKRYRITYGETGNSPVQEFVPPWASITATIS 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1537 VSDVPRDLVIASTPTSLISWEPPAVSVRYRITYGETGNSPVQEFVPGSKSTATIN 1596
QY 61 GLKPGVDYTTTIVAVTDSKDTYKYDDPISINYRT 94
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1597 NIKPGADYTTITVAVTGRGDSPASSKPVSIYQT 1630
RESULT 4
A28512
fibronectin - chicken (fragment)
C;Species: Gallus gallus (Chicken)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A28512
R;Kubomura, S.; Obara, M.; Karasaki, Y.; Taniguchi, H.; Gotoh, S.; Tsuda, T.; Higashi, K.
Biochim. Biophys. Acta 910, 171-181, 1987
A;Title: Genetic analysis of the cell binding domain region of the chicken fibronectin gene
A;Reference number: A28512; MUID:88050950; PMID:2823899
A;Accession: A28512
A;Molecule type: DNA
A;Residues: 1-273 <KUB>
A;Cross-references: UNIPROT:P11722; UNIPARC:UPI000017131E; GB:X06533; NID:G63393; PIDN:CI/
A;Note: the authors translated the codon CCG for residue 190 as Gln, CAG for residue 243
C;Genetics:
A;Introns: 90/1; 129/1; 184/1; 236/1
C;Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat
C;Keywords: alternative splicing; duplication; extracellular matrix; glycoprotein; hetero
F;1-82/Domain: fibronectin type III repeat homology (fragment) <FN3I>
F;90-172/Domain: fibronectin type III repeat homology <FN3J>
F;167-169/Region: cell attachment (R-G-D) motif
F;184-266/Domain: fibronectin type III repeat homology <FN3K>
Query Match 63.0%; Score 311; DB 2; Length 273;
Best Local Similarity 64.9%; Pred. No. 2e-24;
Matches 61; Conservative 11; Mismatches 22; Indels 0; Gaps 0;
QY 1 VSDVPRDLVVAATPTSLRISWNRSGLQSKRYRITYGETGNSPVQEFVPPWASITATIS 60
Db 90 VSDVPRDLVNPSTPSLSISWDAPAVTVRYRITYGETGNSPVQEFVPGTMSRATIT 149
QY 61 GLKPGVDYTTTIVAVTDSKDTYKYDDPISINYRT 94
Db 150 GLKPGVDYTTTIVAVTGRGDSPASSKPVTVTYKT 183
RESULT 5
A29355
fibronectin - chicken (fragment)
C;Species: Gallus gallus (Chicken)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A29355
R;Norton, P.A.; Hynes, R.O.
Mol. Cell. Biol. 7, 4297-4307, 1987
A;Title: Alternative splicing of chicken fibronectin in embryos and in normal and transfe
A;Reference number: A29355; MUID:88142820; PMID:2830487
A;Accession: A29355
A;Molecule type: mRNA
A;Residues: 1-1020 <NOR>
A;Cross-references: UNIPROT:P11722; UNIPARC:UPI0000177AEE
C;Genetics:
A;Introns: 176/3
C;Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-4135 <ELE>
A;Cross-references: UNIPROT:O18977; UNIPARC:UPI00001101C4; EMBL:Y11915; NID:G2462978; PIDN:G2462978
C;Gene: TN-X
C;Superfamily: tenascin-X; EGF homology; fibrinogen beta/gamma homology; fibronectin type I
C;Keywords: extracellular matrix; glycoprotein; heptad repeat

Query Match 25.1%; Score 124; DB 2; Length 4135;
Best Local Similarity 35.9%; Pred. No. 0.00065;
Matches 33; Conservative 17; Mismatches 36; Indels 6; Gaps 3;

QY 3 DVPRDLVVAATPTSLISWNRSLGQSRYYRITYGTGNSPVQETVPPWASIAIISGL 62
DB 840 DGPDLVVAATPTSLISWNRSLGQSRYYRITYGTGNSPVQETVPPWASIAIISGL 897

QY 63 KPGVDYTIIVYAVTDKSDTYKYDDPISINVRT 94
DB 898 MPGVEYVTVTAERGRAVSY----PASIRANT 925

RESULT 9
JH0675
restrictin precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JH0675; PS0385; S23254
R;Noerenberg, U.; Wille, H.; Wolffe, J.M.; Frank, R.; Rathjen, F.G.
Nucleon 8, 849-863, 1992
A;Title: The chicken neural extracellular matrix molecule restrictin: similarity with EG
A;Reference number: JH0675; MUID:92265298; PMID:1375037
A;Accession: JH0675
A;Molecule type: mRNA
A;Residues: 1-1353 <NOE>
A;Cross-references: UNIPROT:Q00546; UNIPARC:UPI00000FC0A7; GB:X64649; NID:G63613; PIDN:G63613
A;Experimental source: brain
A;Accession: PS0385
A;Molecule type: protein
A;Residues: 579-586;827-840 <NOE1>
A;Cross-references: UNIPARC:UPI0000174344; UNIPARC:UPI0000174345
C;Comment: This protein is a neural extracellular matrix protein implicated in neural ce
C;Superfamily: restrictin; EGF homology; fibrinogen beta/gamma homology; fibronectin typ
C;Keywords: calcium binding; cell adhesion; duplication; extracellular matrix; glycopro
F;1-33/Domain: signal sequence #status predicted <SIG>
F;203-229/Domain: restrictin #status predicted <MAT>
F;34-1353/Product: restrictin #status predicted <SIG>
F;234-260/Domain: EGF homology <EG1>
F;265-291/Domain: EGF homology <EG2>
F;296-322/Domain: EGF homology <EG3>
F;324-405/Domain: fibronectin type III repeat homology <FN1>
F;413-494/Domain: fibronectin type III repeat homology <FN2>
F;502-584/Domain: fibronectin type III repeat homology <FN3>
F;592-676/Domain: fibronectin type III repeat homology <FN4>
F;684-764/Domain: fibronectin type III repeat homology <FN5>
F;762-853/Domain: fibronectin type III repeat homology <FN6>
F;861-941/Domain: fibronectin type III repeat homology <FN7>
F;1035-1115/Domain: fibronectin type III repeat homology <FN8>
F;1130-1338/Domain: fibronectin type III repeat homology <FN9>
F;1270-1286/Region: calcium binding #status predicted
F;1272-1286/Region: calcium binding #status predicted
F;53,197,277,391,469,580,734,790,960,1031,1041,1236,1342/Binding site: carbohydrate (Aer

Query Match 24.5%; Score 121; DB 1; Length 1353;
Best Local Similarity 40.3%; Pred. No. 0.00037;
Matches 29; Conservative 13; Mismatches 28; Indels 2; Gaps 1;

QY 3 DVPRDLVVAATPTSLISWNRSLGQSRYYRITYGTGNSPVQETVPPWASIAIISGL 62
DB 686 DSPRDLVVAATPTSLISWNRSLGQSRYYRITYGTGNSPVQETVPPWASIAIISGL 743

QY 63 KPGVDYTIIVYAVTDKSDTYKYDDPISINVRT 94

DB 744 EPGTEYTIISIIA 755

RESULT 10
S19694
tenascin precursor - pig
N;Alternate names: contactin; hexabrachion
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S19694
R;Nishi, T.; Weinstein, J.; Gillespie, W.M.; Paulson, J.C.
Eur. J. Biochem. 202, 643-648, 1991
A;Title: Complete primary structure of porcine tenascin. Detection of tenascin transcrip
A;Reference number: S19694; MUID:92104189; PMID:1722152
A;Accession: S19694
A;Molecule type: mRNA
A;Residues: 1-1746 <NIS>
A;Cross-references: UNIPROT:Q29116; UNIPARC:UPI0000136BBB; EMBL:X61599; NID:G2124; PIDN:
C;Superfamily: tenascin; EGF homology; fibrinogen beta/gamma homology; fibronectin type I
C;Keywords: alternative splicing; calcium binding; cell adhesion; duplication; extracell
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-1746/Product: tenascin #status predicted <MAT>
F;346-372/Domain: EGF homology <EGF>
F;377-403/Domain: EGF homology <EGF2>
F;622-703/Domain: fibronectin type III repeat homology <FN3A>
F;711-793/Domain: fibronectin type III repeat homology <FN3B>
F;802-884/Domain: fibronectin type III repeat homology <FN3C>
F;892-976/Domain: fibronectin type III repeat homology <FN3D>
F;984-1064/Domain: fibronectin type III repeat homology <FN3E>
F;1073-1155/Domain: fibronectin type III repeat homology <FN3F>
F;1164-1246/Domain: fibronectin type III repeat homology <FN3G>
F;1254-1335/Domain: fibronectin type III repeat homology <FN3H>
F;1343-1423/Domain: fibronectin type III repeat homology <FN3I>
F;1431-1511/Domain: fibronectin type III repeat homology <FN3J>
F;1526-1734/Domain: fibrinogen beta/gamma homology <FBG>
F;38,166,184,327,788,1034,1079,1121,1354/Binding site: carbohydrate (Aen) (covalent) #sta
Query Match 24.5%; Score 121; DB 1; Length 1746;
Best Local Similarity 35.1%; Pred. No. 0.0005;
Matches 33; Conservative 14; Mismatches 41; Indels 6; Gaps 3;

QY 3 DVPRDLVVAATPTSLISWNRSLGQSRYYRITYGTGG--NSPVOEFTVPPWASIAIIS 60
DB 894 DAPRDLRISQDNTSLISWNRSLGQSRYYRITYGTGG--NSPVOEFTVPPWASIAIIS 953

QY 61 GLKPGVDYTIIVYAVTDKSDTYKYDDPISINVRT 94
DB 954 GLRPGTEYIGVGSVAV--KGD--KESDPATINAA 983

RESULT 11
A45445
janusin precursor, long form - rat
N;Alternate names: neural recognition glycoprotein J1-160/180, long form
N;Contains: neural recognition glycoprotein J1-160/180, short form
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A45445; B45445; S32023
R;Fuss, B.; Wintergerst, E.S.; Bartsch, U.; Schachner, M.
J. Cell Biol. 120, 1237-1249, 1993
A;Title: Molecular characterization and in situ mRNA localization of the neural recognit
A;Reference number: A45445; MUID:93171267; PMID:7679676
A;Accession: A45445
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1356 <FUS>
A;Cross-references: UNIPROT:Q05546; UNIPARC:UPI00000E6D8A; GB:Z18630; NID:G57961; PIDN:G
A;Accession: B45445
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-772,863-1356 <FU2>
A;Cross-references: UNIPARC:UPI0000177AF2; GB:Z18630
R;Fuss, B.; Wintergerst, E.; Bartsch, U.; Schachner, M.

submitted to the EMBL Data Library, November 1992

A;Description: Molecular characterization and in situ mRNA localization of the neural re

A;Reference number: S32023

A;Accession: S32023

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-1356 <FUS2>

A;Cross-references: UNIPARC:UPI000006D8A; EMBL:Z18630; NID:g57961; PIDN:CAA79229.1; PID

A;Superfamily: restrictin; EGF homology; fibrinogen beta/gamma homology; fibronectin tyf

C;Keywords: alternative splicing; duplication; fibronectin type III repeat homology; olig

F;1-1356/Product: janusin, long form #status experimental <ALT>

F;1-772,863-1356/Product: janusin, short form #status experimental <ALT>

F;204-230/Domain: EGF homology <EG1>

F;235-261/Domain: EGF homology <EG2>

F;266-292/Domain: EGF homology <EG3>

F;297-323/Domain: EGF homology <EG4>

F;325-405/Domain: fibronectin type III repeat homology <FN1>

F;413-494/Domain: fibronectin type III repeat homology <FN2>

F;502-584/Domain: fibronectin type III repeat homology <FN3>

F;592-676/Domain: fibronectin type III repeat homology <FN4>

F;684-764/Domain: fibronectin type III repeat homology <FN5>

F;772-854/Domain: fibronectin type III repeat homology <FN6>

F;1038-1118/Domain: fibronectin type III repeat homology <FN7>

F;1133-1341/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 23.5%; Score 116; DB 2; Length 1356;

Best Local Similarity 27.4%; Pred. No. 0.0012;

Matches 34; Conservative 18; Mismatches 36; Indels 36; Gaps 3;

QY 3 DVPRDLVVAATPTSLRISLNRSGLQSYRYITVGETGNSPVQVFTVPPWASIIATISGL 62

Db 686 DSPRLDMVTASSETSLIWTKASGPIDHYRITPTSSGIS--SEVTVPRDRSTYTUTDL 743

QY 63 KPGVDYITVYA-----VTDKSDTYKYDDP-----I 88

Db 744 EPGAEEYIISIAERGRQOQSLSTVDAFTGPRFPIHSHFHSVNTSSVNIWSPSPADRL 803

QY 89 SINY 92

Db 804 ILNY 807

RESULT 12

A40701

tenascin-X precursor - human

C;Species: Homo sapiens (man)

C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 31-Dec-2004

C;Accession: A40701; A33725; C42175

R;Bristow, J.; Tee, M.K.; Gitelman, S.E.; Mellon, S.H.; Miller, W.L.

J. Cell Biol. 122, 265-278, 1993

A;Title: Tenascin-X: a novel extracellular matrix protein encoded by the human XB gene c

A;Reference number: A40701; MUID:93300909; PMID:7686164

A;Accession: A40701

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-3566 <BRI>

A;Cross-references: UNIPROT:P22105; UNIPROT:Q9UC11; UNIPARC:UPI0000174343; EMBL:X71937

R;Morel, Y.; Bristow, J.; Gitelman, S.E.; Miller, W.L.

Proc. Natl. Acad. Sci. U.S.A. 86, 6582-6586, 1989

A;Title: Transcript encoded on the opposite strand of the human steroid 21-hydroxylase/c

A;Reference number: A33725; MUID:69367293; PMID:2475872

A;Accession: A33725

A;Molecule type: mRNA

A;Residues: 2748-3199, 'V', 3201-3298, 'E', 3299-3314, 'G', 3316-3566 <MOR>

A;Cross-references: UNIPARC:UPI000016A98B; GB:M25813; NID:g183069; PIDN:AAA35884.1; PID:

R;Matsumoto, K.; Arai, M.; Ishihara, N.; Ando, A.; Inoko, H.; Ikemura, T.

Genomics 12, 485-491, 1992

A;Title: Cluster of fibronectin type III repeats found in the human major histocompatib

enacin.

A;Reference number: A42175; MUID:92217969; PMID:1373119

A;Accession: C42175

A;Molecule type: DNA

A;Residues: 1849-1936 <MAT>

A;Cross-references: UNIPARC:UPI000006F862

A;Experimental source: clone 3.9kF3-1

A;Note: sequence extracted from NCBI backbone (NCBIP:95694)

C;Genetics:

A;Gene: GDB:TNXA; D6S103E; TNX; XA; XB

A;Cross-references: GDB:568487; OMIM:600261

A;Map position: 6p21.3-6p21.3

C;Superfamily: EGF homology; fibrinogen beta/gamma homology; fibronectin type III repeat

C;Keywords: extracellular matrix; glycoprotein

F;435-461/Domain: EGF homology <EGF>

F;748-828/Domain: fibronectin type III repeat homology <3F1>

F;829-856/Domain: fibronectin type III repeat homology #status atypical <3F2>

F;873-953/Domain: fibronectin type III repeat homology <3F3>

F;975-1055/Domain: fibronectin type III repeat homology <3F4>

F;1078-1158/Domain: fibronectin type III repeat homology <3F5>

F;1167-1247/Domain: fibronectin type III repeat homology <3F6>

F;1248-1317/Domain: fibronectin type III repeat homology #status atypical <3F7>

F;1323-1403/Domain: fibronectin type III repeat homology <3F8>

F;1412-1492/Domain: fibronectin type III repeat homology <3F9>

F;1510-1590/Domain: fibronectin type III repeat homology <3F10>

F;1618-1676/Domain: fibronectin type III repeat homology #status atypical <3F11>

F;1678-1749/Domain: fibronectin type III repeat homology #status atypical <3F12>

F;1751-1831/Domain: fibronectin type III repeat homology <3F13>

F;1849-1929/Domain: fibronectin type III repeat homology <3F14>

F;1955-2035/Domain: fibronectin type III repeat homology <3F15>

F;2061-2141/Domain: fibronectin type III repeat homology <3F16>

F;2167-2246/Domain: fibronectin type III repeat homology <3F17>

F;2274-2354/Domain: fibronectin type III repeat homology <3F18>

F;2382-2462/Domain: fibronectin type III repeat homology <3F19>

F;2488-2568/Domain: fibronectin type III repeat homology <3F20>

F;2584-2664/Domain: fibronectin type III repeat homology <3F21>

F;2677-2757/Domain: fibronectin type III repeat homology <3F22>

F;2771-2851/Domain: fibronectin type III repeat homology <3F23>

F;2878-2958/Domain: fibronectin type III repeat homology <3F24>

F;2977-3067/Domain: fibronectin type III repeat homology #status atypical <3F25>

F;3078-3159/Domain: fibronectin type III repeat homology <3F26>

F;3167-3247/Domain: fibronectin type III repeat homology <3F27>

F;3255-3334/Domain: fibronectin type III repeat homology <3F28>

F;3349-3557/Domain: fibrinogen beta/gamma homology <FBG>

Query Match 22.5%; Score 111; DB 1; Length 3566;

Best Local Similarity 31.9%; Pred. No. 0.012;

Matches 30; Conservative 18; Mismatches 40; Indels 6; Gaps 3;

QY 1 VSDVPRDLVVAATPTSLRISLNRSGLQSYRYITVGETGNSPVQVFTVPPWASIIATIS 60

Db 748 VIDGPQDLRVSVVSTPTTLEGLWLRPQAEVDFRVVSV--VSADNQRVR-LEVPFETDGTLLT 805

QY 61 GLKPGVDYITTVVAVTDKSDTYKYDDPISINVRT 94

Db 806 DLMPGVEYVTVTAERGRAVSY----PASVRANT 835

RESULT 13

S46216

leukocyte antigen-related protein precursor - rat

N;Alternate names: leukocyte common antigen homolog

N;Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text_change 09-Jul-2004

C;Accession: S46216; S23252; A41032; A33154

R;Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.

Biochem. J. 302, 39-47, 1994

A;Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-pho

A;Reference number: S46216; MUID:94347119; PMID:8068021

A;Accession: S46216

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-1898 <ZHA>

A;Cross-references: UNIPROT:Q64604; UNIPARC:UPI0000087A8; EMBL:L11586; NID:g205132; PID

R;Hashimoto, N.; Zhang, W.R.; Goldstein, B.J.

Biochem. J. 284, 569-576, 1992

A;Title: Insulin receptor and epidermal growth factor receptor dephosphorylation by three

RESULT 15

```

A31930
Cytotactin - chicken (fragments)
C:Species: Gallus gallus (Chicken)
C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 09-Jul-2004
C:Accession: A31930
R:Jones, F.S.; Burgoon, M.P.; Hoffman, S.; Crossin, K.L.; Cunningham, B.A.; Edelman, G.M.
Proc. Natl. Acad. Sci. U.S.A. 85, 2186-2190, 1988
A:Title: A cDNA clone for cytotactin contains sequences similar to epidermal growth factor
A:Reference number: A31930; MUID:88176910; PMID:2451243
A:Accession: A31930
A:Molecule type: mRNA
A:Residues: 1-933 <JON>
A:Cross-references: UNIPROT:PI0039; UNIPARC:UPI0000177AF5
A:Note: the authors' translation of the codons for residues 601-620 differs considerably
C:Superfamily: tenascin; EGF homology; fibronogen beta/gamma homology; fibronectin type
C:Keywords: alternative splicing; glycoprotein
F:13-39/Domain: EGF homology <EGF>
F:134-215/Domain: fibronectin type III repeat homology <FN3A>
F:223-307/Domain: fibronectin type III repeat homology <FN3B>
F:315-399/Domain: fibronectin type III repeat homology <FN3C>
F:407-491/Domain: fibronectin type III repeat homology <FN3D>
F:499-576/Domain: fibronectin type III repeat homology <FN3E>
F:587-668/Domain: fibronectin type III repeat homology <FN3F>
F:765-845/Domain: fibronectin type III repeat homology <FN3G>
F:860-933/Domain: fibronogen beta/gamma homology (fragment) <FBG>
F:145,185,293,301,676,688/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 21.9%; Score 108; DB 2; Length 933;
Best Local Similarity 33.7%; Pred. No. 0.0052;
Matches 32; Conservative 13; Mismatches 42; Indels 8; Gaps 3;

Qy 3 DVPRDLVVAATPTSLRISWNRSGLQSRYYRITYGETGNSPVQEEFTVPPW---ASIAITI 59
Db 409 DAPENLKRVSQTDNSITLEWKFPSHANIDNRYIKFAPISGDDHT-ELTVPKGNQATRTL 467

Qy 60 SGLKPGVDYTIIVYAVTDKSDTYKYDDPISINVRT 94
Db 468 TGLRPGTEYIGIVTAVRQDRES----APATINAGT 498

```

Search completed: February 23, 2006, 07:48:17
Job time : 40 secs

This page blank (uspto)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2006, 07:40:29 ; Search time 228 Seconds
(without alignments)
290.876 Million cell updates/sec

Title: US-09-688-566-81
Perfect score: 494
Sequence: 1 VSDVPRDLVVAATPTSLRI.....VTDKSDTYKYDDPISINRYT 94

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	361	73.1	787	2	Q5CZ99 HUMAN
2	361	73.1	1011	2	Q5G222 HUMAN
3	361	73.1	1034	2	Q6N084 HUMAN
4	361	73.1	1255	2	Q6MZS0 HUMAN
5	361	73.1	2146	2	Q68CX6 HUMAN
6	361	73.1	2217	2	Q585T2 HUMAN
7	361	73.1	2240	2	Q68DP8 HUMAN
8	361	73.1	2265	2	Q60FE4 HUMAN
9	361	73.1	2267	2	Q68DP9 HUMAN
10	361	73.1	2296	2	Q6N0A6 HUMAN
11	361	73.1	2351	2	Q59EH1 HUMAN
12	361	73.1	2357	2	Q68D74 HUMAN
13	361	73.1	2386	1	FINC HUMAN
14	361	73.1	2444	2	Q6N025 HUMAN
15	361	73.1	2477	2	Q6MZU5 HUMAN
16	356	72.1	2193	2	Q6MZM7 HUMAN
17	354	71.7	2265	1	FINC BOVIN
18	333	67.4	2477	1	FINC MOUSE
19	333	67.4	2477	1	FINC RAT
20	311	63.0	1256	1	FINC CHICK
21	269	54.5	293	2	Q9XSG0 RABIT
22	264	53.4	1328	2	FINC FLEWA
23	262	53.0	2481	1	FINC XENLA
24	262	53.0	2481	2	Q6GQA5 XENLA
25	254	51.4	2383	2	Q4RNC4 TETNG
26	254	51.4	2475	2	Q501R6 XENOPUS
27	251	50.8	2478	2	Q93406 BRACHYDANIO
28	246	49.8	2408	2	Q6JANZ BRACHYDANIO
29	246	49.8	2500	2	Q58XP5 BRACHYDANIO
30	153	31.0	68	2	Q28692 ORYCTOLAGUS
31	130	26.3	522	1	FINC HORSE

32	125	25.3	4006	2	O35452	MUS MUSCULU
33	125	25.3	4114	2	O54796	MUS MUSCULU
34	124	25.1	4135	2	O18977	BOS TAURUS
35	123	24.9	320	2	Q95KV4	BOS TAURUS
36	123	24.9	347	2	Q95KV5	BOS TAURUS
37	123	24.9	426	2	Q9NPK8	HOMO SAPIEN
38	123	24.9	522	1	FINC CANFA	Q28275 CANIS FAMIL
39	123	24.9	1350	2	Q7T3T6	BRACHYDANIO
40	123	24.9	4222	2	Q5ST74	HOMO SAPIEN
41	123	24.9	4222	2	Q5SQD3	HOMO SAPIEN
42	123	24.9	4288	2	Q9NPK9	HOMO SAPIEN
43	123	24.9	4289	1	TENX HUMAN	P22105 HOMO SAPIEN
44	122	24.7	354	2	Q9UQ56	HOMO SAPIEN
45	122	24.7	379	2	O95617	HOMO SAPIEN

ALIGNMENTS

RESULT 1
Q5CZ99_HUMAN PRELIMINARY; PRT; 787 AA.
AC Q5CZ99;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Hypothetical protein DKFZp686I1370 (Fragment).
GN Name=DKFZp686I1370;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Endometrium carcinoma cell line;
RG The German CDNA Consortium;
RA Ansorge W., Krieger S., Regiert T., Rittmuller C., Schwager B.,
RA Mewes H.W., Weil B., Amid C., Oeanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR936623; CA156766.1; -, mRNA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003961; FN_III.
DR PRINTS; PR00014; FNTYPEIII.
DR SMART; SM00060; FN3; 8.
DR PROSITE; PS00687; ALDEHYDE DEHYDR_GLU; UNKNOWN_1.
DR PROSITE; PS00853; FN3; 9.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 787 AA; 85622 MW; 5B49003169158ADD CRC64;

Query Match 73.1%; Score 361; DB 2; Length 787;
Best Local Similarity 77.7%; Pred. No. 2.4e-30;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLVVAATPTSLRI...VTDKSDTYKYDDPISINRYT 94
Db 237 VSDVPRDLVVAATPTSLRI...VTDKSDTYKYDDPISINRYT 330

Qy 61 GLKPGVDYTTIVAVTDKSDTYKYDDPISINRYT 94
Db 297 GLKPGVDYTTIVAVTDKSDTYKYDDPISINRYT 330

RESULT 2

Q5G222_HUMAN PRELIMINARY; PRT; 1011 AA.
AC Q5G222;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)

Fibronectin 1 variant (Fragment).
GN Name=Fibronectin 1 variant;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno F.R.;
RA "None Title."; RT
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
RE EMBL; AB209287; BAD92524.1; -, mRNA.
FT NON TER 1
SQ SEQUENCE 1011 AA; 110893 MW; 40CAF97C3023248D CRC64;
Query Match 73.1%; Score 361; DB 2; Length 1011;
Best Local Similarity 77.7%; Pred. No. 3.2e-30;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;
Qy 1 VSDVPRDLVVAAATPTSLRISWNRSGLQSRYYRITYGETGNSPVQSFVTPPWASIAITIS 60
Db 193 VSDVPRDLVVAAATPTSLISWDPAPVTYRITYGETGNSPVQSFVTPVSGSKSTATIS 252
Qy 61 GLKPGVDTITVYAVTDKSDTYKYDDPISINYRT 94
Db 253 GLKPGVDTITVYAVTGRGDSPASSKPSISINYRT 286
RESULT 3
Q6N084_HUMAN
ID Q6N084_HUMAN PRELIMINARY; PRT; 1034 AA.
AC Q6N084;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFP686L11144 (Fragment).
GN Name=DKFP686L11144;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RC TISSUE=Human colon endothel primary cell culture;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX540638; CA545786.1; -, mRNA.
DR SMR; Q6N084; 1-309, 402-670.
DR GO; GO:0005576; C:extracellular region; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR006209; EGF like
DR InterPro; IPR000083; Fibrinctnl.
DR InterPro; IPR003962; FnIII subd.
DR InterPro; IPR003961; FN III.
DR Pfam; PF00039; fn1; 3.
DR Pfam; PF00041; fn3; 8.
DR PRINTS; PR00012; FNTYPEI.
DR PRINTS; PR00014; FNTYPEIII.
DR SMART; SM00058; fn1; 3.
DR SMART; SM00060; fn3; 8.
DR PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN 1.
DR PROSITE; PS00022; EGF 1; UNKNOWN 1.
DR PROSITE; PS01253; FIBRONECTIN 1; 3.
DR PROSITE; PS00853; fn3; 9.
DR KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 1034 AA; 113371 MW; 3765128365FD0659 CRC64;

```
AC Q68CX6;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein DKFZp686O13149.
GN Name=DKFZp686O13149;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Wilson R.K.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC012462; AAX76513.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 2217
SQ SEQUENCE 2217 AA; 243438 MW; FAF1D07FBB6C44E5 CRC64;

Query Match 73.1%; Score 361; DB 2; Length 2217;
Best Local Similarity 77.7%; Pred. No. 8.3e-30;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISWNSRGLQSYRYITYGTGNSPVQSFVPPWASIIATIS 60
DB 1447 VSDVPRDLEVAATPTSLISWNSRGLQSYRYITYGTGNSPVQSFVPPWASIIATIS 1506
QY 61 GLKPGVDYTTTVAATDKSTYKYDDPISINVRT 94
DB 1507 GLKPGVDYTTTVAATDKSTYKYDDPISINVRT 1540

RESULT 7
Q68DP8 HUMAN
ID Q68DP8_HUMAN PRELIMINARY; PRT; 2240 AA.
AC Q68DP8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Hypothetical protein DKFZp686H0342.
GN Name=DKFZp686H0342;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Wasserstrom R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Wasserstrom R.;
RL Submitted (APR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC012462; AAX76513.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 2217
SQ SEQUENCE 2217 AA; 243438 MW; FAF1D07FBB6C44E5 CRC64;

Query Match 73.1%; Score 361; DB 2; Length 2146;
Best Local Similarity 77.7%; Pred. No. 8e-30;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISWNSRGLQSYRYITYGTGNSPVQSFVPPWASIIATIS 60
DB 165 VSDVPRDLEVAATPTSLISWNSRGLQSYRYITYGTGNSPVQSFVPPWASIIATIS 224
QY 61 GLKPGVDYTTTVAATDKSTYKYDDPISINVRT 94
DB 225 GLKPGVDYTTTVAATDKSTYKYDDPISINVRT 258

RESULT 6
Q585T2 HUMAN
ID Q585T2_HUMAN PRELIMINARY; PRT; 2217 AA.
AC Q585T2;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Hypothetical protein FN1 (Fragment).
GN Name=FN1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.H.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
```

—

DE Hypothetical protein DKF2p686M04163.
GN Name=DKF2p686M04163;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE
RC TISSUE=uterus endothel;
RG The German cDNA Consortium;
RA Bloecher H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: BX640608; CA845714.1; -; mRNA.
DR GO: G0:0005576; C:extracellular region; IEA.
DR InterPro: IPR002086; ALDEHYD DEHYDR.
DR InterPro: IPR006209; EGF like.
DR InterPro: IPR000083; Fibrinctnl.
DR InterPro: IPR003962; FNIII subd.
DR InterPro: IPR003961; FN III.
DR InterPro: IPR000562; FN_Type_II.
DR Pfam: PF00039; fn1; 12.
DR Pfam: PF00040; fn2; 2.
DR Pfam: PF00041; fn3; 15.
DR PRINTS: PR00012; FNTYPEI.
DR PRINTS: PR00013; FNTYPEII.
DR PRINTS: PR00014; FNTYPEIII.
DR ProDom: PD000995; FN_Type_II; 2.
DR SMART: SM00058; FN1; 12.
DR SMART: SM00059; FN2; 2.
DR SMART: SM00060; FN3; 15.
DR PROSITE: PS00687; ALDEHYDE DEHYDR_GLU; UNKNOWN_1.
DR PROSITE: PS00022; EGF_1; UNKNOWN_2.
DR PROSITE: PS01253; FIBRONECTIN_1; 12.
DR PROSITE: PS00023; FIBRONECTIN_2; 2.
DR PROSITE: PS00853; FN3; 15.
KW Hypothetical protein.
SQ SEQUENCE 2296 AA; 252761 MW; 9AB2D723CC0CED70 CRC64;

Query Match 73.1%; Score 361; DB 2; Length 2296;
Best Local Similarity 77.7%; Pred. No. 8.6e-30;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISWNRSGLQSYRYITYGTGNSPVQSFYPPWASIIATIS 60
DB 1447 VSDVPRDLEVAATPTSLISWDAPAVTVRYITYGTGNSPVQSFYPPWASIIATIS 1506

QY 61 GLKPGVDYTTTVAVTDKSTYKYDDPISINRYT 94
DB 1507 GLKPGVDYTTTVAVTCGRGSPASSKPIISINRYT 1540

RESULT 11
Q59EH1_HUMAN PRELIMINARY; PRT; 2351 AA.
AC Q59EH1
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Fibronectin 1 variant (Fragment).
GN Name=Fibronectin 1 variant;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Aorta endothelial cell;
RA Totoki Y., Toyoda A., Takeda T., Sakaki Y., Tanaka A., Yokoyama S.,
RA Ohara O., Nagase T., Kikuno F.R.;
RT "None Title";

RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB209840; BAD93077.1; -; mRNA.
FT NON_TER 1 1
SQ SEQUENCE 2351 AA; 258611 MW; 67149C626199075E CRC64;

Query Match 73.1%; Score 361; DB 2; Length 2351;
Best Local Similarity 77.7%; Pred. No. 8.9e-30;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISWNRSGLQSYRYITYGTGNSPVQSFYPPWASIIATIS 60
DB 1533 VSDVPRDLEVAATPTSLISWDAPAVTVRYITYGTGNSPVQSFYPPWASIIATIS 1592

QY 61 GLKPGVDYTTTVAVTDKSTYKYDDPISINRYT 94
DB 1593 GLKPGVDYTTTVAVTCGRGSPASSKPIISINRYT 1626

RESULT 12
Q68DT4_HUMAN PRELIMINARY; PRT; 2357 AA.
AC Q68DT4
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein DKF2p686F10164.
GN Name=DKF2p686F10164;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Uterus endothel;
RG The German cDNA Consortium;
RA Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: CR749281; CAH18136.1; -; mRNA.
DR GO: G0:0005576; C:extracellular region; IEA.
DR GO: G0:0016491; F:oxidoreductase activity; IEA.
DR GO: G0:0008152; P:metabolism; IEA.
DR InterPro: IPR002086; ALDEHYD DEHYDR.
DR InterPro: IPR006209; EGF like.
DR InterPro: IPR000083; Fibrinctnl.
DR InterPro: IPR003961; FN III.
DR InterPro: IPR000562; FN_Type_II; 2.
DR Pfam: PF00039; fn1; 12.
DR Pfam: PF00040; fn2; 2.
DR Pfam: PF00041; fn3; 15.
DR PRINTS: PR00012; FNTYPEI.
DR PRINTS: PR00013; FNTYPEII.
DR PRINTS: PR00014; FNTYPEIII.
DR ProDom: PD000995; FN_Type_II; 2.
DR SMART: SM00058; FN1; 12.
DR SMART: SM00059; FN2; 2.
DR SMART: SM00060; FN3; 15.
DR PROSITE: PS00687; ALDEHYDE DEHYDR_GLU; 1.
DR PROSITE: PS00022; EGF_1; 2.
DR PROSITE: PS01253; FN1_1; 12.
DR PROSITE: PS1091; FN1_2; 12.
DR PROSITE: PS00023; FN2_1; 2.
DR PROSITE: PS1092; FN2_2; 2.
DR PROSITE: PS00853; FN3; 15.
KW Hypothetical protein; Repeat.
SQ SEQUENCE 2357 AA; 259092 MW; BEAE3990E27E532A CRC64;

Query Match 73.1%; Score 361; DB 2; Length 2357;
Best Local Similarity 77.7%; Pred. No. 8.9e-30;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

[18]
RP NUCLEOTIDE SEQUENCE OF 1712-1739.
RX MEDLINE=87026578; PubMed=3021206;
RA Sekiguchi K., Klos A.M., Kurachi K., Yoshitake S., Hakomori S.;
RT "Human liver fibronectin complementary DNAs: identification of two
RT different messenger RNAs possibly encoding the alpha and beta subunits
RT of plasma fibronectin.";
RL Biochemistry 25:4936-4941(1986).
[19]
RN NUCLEOTIDE SEQUENCE OF 1788-2386 (ISOFORMS 4; 5 AND 6).
RP TISSUE=Cartilage;
RX MEDLINE=22126816; PubMed=12127832; DOI=10.1053/joca.2002.0792;
RA Parker A.E., Boutell J., Carr A., Maciewicz R.A.;
RT "Novel cartilage-specific splice variants of fibronectin.";
RL Osteoarthritis Cartilage 10:528-534(2002).
[20]
RN NUCLEOTIDE SEQUENCE OF 1948-2067.
RX MEDLINE=85231203; PubMed=2989004; DOI=10.1016/0014-5793(85)81333-8;
RA Umezawa K., Kornblitt A.R., Baralle F.E.;
RT "Isolation and characterization of cDNA clones for human liver
RT fibronectin.";
RL FEBS Lett. 186:31-34(1985).
[21]
RN NUCLEOTIDE SEQUENCE OF 1992-2147.
RX MEDLINE=87030929; PubMed=3770201; DOI=10.1016/0014-5793(86)81506-X;
RA Vibe-Pedersen K., Magnusson S., Baralle F.E.;
RT "Donor and acceptor splice signals within an exon of the human
RT fibronectin gene: a new type of differential splicing.";
RL FEBS Lett. 207:287-291(1986).
[22]
RN PROTEIN SEQUENCE OF 2071-2356 (ISOFORM 3).
RX MEDLINE=85261459; PubMed=4019516;
RA Garcia-Pardo A., Pearlstein E., Frangione B.;
RT "Primary structure of human plasma fibronectin. Characterization of a
RT 31,000-dalton fragment from the COOH-terminal region containing a free
RT sulphydryl group and a fibrin-binding site.";
RL J. Biol. Chem. 260:10320-10325(1985).
[23]
RN NUCLEOTIDE SEQUENCE OF 2291-2386.
RX PubMed=6304699;
RA Kornblitt A.R., Vibe-Pedersen K., Baralle F.E.;
RT "Isolation and characterization of cDNA clones for human and bovine
RT fibronectins.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:3218-3222(1983).
[24]
RN PROTEIN SEQUENCE OF 32-290.
RX MEDLINE=84032463; PubMed=6630202;
RA Garcia-Pardo A., Pearlstein E., Frangione B.;
RT "Primary structure of human plasma fibronectin. The 29,000-dalton NH2-
RT terminal domain.";
RL J. Biol. Chem. 258:12670-12674(1983).
[25]
RN MEDLINE=86042625; PubMed=2414772;
RX MEDLINE=87080265; PubMed=3024962;
RA Owens R.J., Baralle F.E.;
RT "Mapping the collagen-binding site of human fibronectin by expression
RT in Escherichia coli.";
RL EMBO J. 5:2825-2830(1986).
[26]
RN SULFATION.
RX MEDLINE=86042625; PubMed=2414772;
RA Liu M.C., Yu S., Sy J., Redman C.M., Lipmann F.;
RT "Tyrosine sulfation of proteins from the human hepatoma cell line
RT HepG2.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:7160-7164(1985).
Query Match 73.1%; Score 361; DB 1; Length 2386;
Best Local Similarity 77.7%; Pred. No. 9e-30;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;
QY 1 VSDVPRDLVVAATPTSLISWDAFVTVYRITYTGCGNSPVQEFVPPWASIAIIS 60
DB 1447 VSDVPRDLVVAATPTSLISWDAFVTVYRITYTGCGNSPVQEFVPPWASIAIIS 1506

QY 61 GLKPGVDYTTIVAVTDKSDTKYKDDPISINYRT 94
DB 1507 GLKPGVDYTTIVAVTGRGDSPASSKPFISINYRT 1540
RESULT 14
Q6N025_HUMAN
ID Q6N025_HUMAN PRELIMINARY; PRT; 2444 AA.
AC Q6N025; 2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686M2451 (Fragment).
GN Name=DKFZp686M2451;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Theria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human endometrium carcinoma cell line;
RA The German Human cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX40731; CA545847.1; -, mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR000083; Fibrinctn1.
DR InterPro; IPR003962; FnIII subd.
DR InterPro; IPR003961; FnIII.
DR InterPro; IPR000562; FN_type_II.
DR Pfam; PF00039; fn1; 12.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 16.
DR PRINTS; PR00012; FNTYPEI.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00014; FNTYPEIII.
DR ProDom; PD000995; FN_type_II; 2.
DR SMART; SM00058; FN1; 12.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 16.
DR PROSITE; PS00687; ALDEHYDE DEHYD GLU; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_2.
DR PROSITE; PS01253; FIBRONECTIN_1; 12.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
DR PROSITE; PS00853; FN3; 16.
KW Hypothetical protein.
FT NON-TER 1
SQ SEQUENCE 2444 AA; 268676 MW; 71C5E8C56A84C7BC CRC64;
Query Match 73.1%; Score 361; DB 2; Length 2444;
Best Local Similarity 77.7%; Pred. No. 9.3e-30;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;
QY 1 VSDVPRDLVVAATPTSLISWDAFVTVYRITYTGCGNSPVQEFVPPWASIAIIS 60
DB 1536 VSDVPRDLVVAATPTSLISWDAFVTVYRITYTGCGNSPVQEFVPPWASIAIIS 1595
QY 61 GLKPGVDYTTIVAVTDKSDTKYKDDPISINYRT 94
DB 1596 GLKPGVDYTTIVAVTGRGDSPASSKPFISINYRT 1629
RESULT 15
Q6MZU5_HUMAN
ID Q6MZU5_HUMAN PRELIMINARY; PRT; 2477 AA.
AC Q6MZU5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFp686O1166.
GN Name=DKFp686O1166;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Endometrium carcinoma cell line;
RG The German cDNA Consortium;
RA Bloeker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Oeanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640875; CAE45932.1; -; mRNA.
DR GO; GO:0005576; C:extracellular region; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR06209; EGF_like.
DR InterPro; IPR000083; Fibrinctnl.
DR InterPro; IPR003962; FnIII_subd.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR000562; FN_Type_II.
DR Pfam; PF00039; fn1; 12.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 17.
DR PRINTS; PR00012; FNTYPEI.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00014; FNTYPEIII.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 12.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 17.
DR PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN 1.
DR PROSITE; PS00022; EGF 1; UNKNOWN 2.
DR PROSITE; PS01253; FIBRONECTIN 1; 12.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
DR PROSITE; PS50853; FN3; 17.
KW Hypothetical protein.
SQ SEQUENCE 2477 AA; 272335 MW; D358D85C6B18207C CRC64;

Query Match 73.1%; Score 361; DB 2; Length 2477;
Best Local Similarity 77.7%; Pred. No. 9.5e-30;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVVAATPTSLISWNRSGLQSRYYRITYGETGNSPVQEFVTPPWASITATIS 60
Db 1538 VSDVPRDLEVVAATPTSLISWDAPAVTVRYRITYGETGNSPVQEFVTPGSKSTATIS 1597

QY 61 GLKPGVDYITTVAVTDKSDTYKYDDPISINYRT 94
Db 1598 GLKPGVDYITTVAVTGRGDSPASSKPISINYRT 1631

Search completed: February 23, 2006, 07:47:33
Job time : 230 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2006, 07:40:25 ; Search time 186 Seconds
(without alignments)
222.052 Million cell updates/sec

Title: US-09-688-566-81

Perfect score: 494

Sequence: 1 VSDVPRDLEVAATPTSLRI.....VTDKSDTYKYDDPISINVRT 94

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 21:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*
- 9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	494	100.0	94	5 ABB78898	Abb78898 Tumour ne
2	494	100.0	94	5 ABB78921	Abb78921 Tumour ne
3	489	99.0	94	5 ABB78939	Abb78939 Tumour ne
4	489	99.0	94	5 ABB78919	Abb78919 Tumour ne
5	489	99.0	94	5 ABB78920	Abb78920 Tumour ne
6	488	98.8	94	5 ABB78911	Abb78911 Tumour ne
7	486	98.4	94	5 ABB78915	Abb78915 Tumour ne
8	484	98.0	94	5 ABB78940	Abb78940 Tumour ne
9	484	98.0	94	5 ABB78912	Abb78912 Tumour ne
10	483	97.8	94	5 ABB78916	Abb78916 Tumour ne
11	483	97.8	94	5 ABB78918	Abb78918 Tumour ne
12	481	97.4	94	5 ABB78899	Abb78899 Tumour ne
13	478	96.8	94	5 ABB78917	Abb78917 Tumour ne
14	463	93.7	94	5 ABB78922	Abb78922 Tumour ne
15	446	90.3	94	5 ABB78923	Abb78923 Tumour ne
16	443	89.7	94	5 ABB78949	Abb78949 Tumour ne
17	439	88.9	94	5 ABB78873	Abb78873 Tumour ne
18	437.5	88.6	93	5 ABB78869	Abb78869 Tumour ne
19	437	88.5	93	5 ABB78868	Abb78868 Tumour ne
20	431	87.2	94	5 ABB78872	Abb78872 Tumour ne
21	419	84.8	94	5 ABB78942	Abb78942 Tumour ne
22	417	84.4	94	5 ABB78870	Abb78870 Tumour ne
23	416	84.2	94	5 ABB78900	Abb78900 Tumour ne
24	415	84.0	94	5 ABB78871	Abb78871 Tumour ne

25	406	82.2	94	5 ABB78895	Abb78895 Tumour ne
26	402	81.4	94	5 ABB78941	Abb78941 Tumour ne
27	397	80.4	94	5 ABB78901	Abb78901 Tumour ne
28	395	80.0	76	5 ABB78897	Abb78897 Tumour ne
29	393	79.6	94	5 ABB78880	Abb78880 Tumour ne
30	392	79.4	94	5 ABB78879	Abb78879 Tumour ne
31	392	79.4	94	5 ABB78928	Abb78928 Tumour ne
32	390	78.9	94	5 ABB78954	Abb78954 Tumour ne
33	390	78.9	94	5 ABB78910	Abb78910 Tumour ne
34	389	78.7	94	5 ABB78881	Abb78881 Tumour ne
35	389	78.7	94	5 ABB78909	Abb78909 Tumour ne
36	388	78.5	94	5 ABB78950	Abb78950 Tumour ne
37	388	78.5	94	5 ABB78876	Abb78876 Tumour ne
38	387.5	78.4	93	5 ABB78896	Abb78896 Tumour ne
39	385	77.9	94	5 ABB78864	Abb78864 Tumour ne
40	384	77.7	94	5 ABB78867	Abb78867 Tumour ne
41	384	77.7	94	5 ABB78904	Abb78904 Tumour ne
42	382.5	77.4	93	5 ABB78878	Abb78878 Tumour ne
43	382	77.3	94	5 ABB78877	Abb78877 Tumour ne
44	380	76.9	94	5 ABB78866	Abb78866 Tumour ne
45	374	75.7	94	5 ABB78929	Abb78929 Tumour ne

ALIGNMENTS

RESULT 1
ABB78898
ID ABB78898 standard; peptide; 94 AA.
XX
AC ABB78898;
XX
DT 30-JUL-2002 (first entry)
XX
DE Tumour necrosis factor-alpha binding amino acid sequence T10.06.
XX
KW Protein scaffold; antibody; binding protein; immunoglobulin;
XX tumour necrosis factor alpha; TNF-alpha; protein framework.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
PN WO200232925-A2.
XX
PD 25-APR-2002.
XX
PF 16-OCT-2001; 2001WO-US032233.
XX
PR 16-OCT-2000; 2000US-00688566.
XX
PA (PHYL-) PHYLLOS INC.
XX
PI Lipovsek D, Wagner RW, Kuimelis RG;
XX
DR WPI; 2002-444238/47.
XX
PT New non-antibody proteins having an immunoglobulin fold, useful in
PT research, therapeutic or diagnostic fields, particularly as scaffolds for
PT designing proteins with specific properties, e.g. for binding any antigen
PT of interest.
XX
PS Claim 47; Fig 25; 94pp; English.
XX
CC The present invention describes a non-antibody protein, comprising a
CC domain having an immunoglobulin-like fold, derived from a reference
CC protein having a mutated amino acid sequence, where the non-antibody
CC protein binds with a Kd at least as tight as 10 nM to a compound that is
CC not bound as tightly by the reference protein. The non-antibody protein
CC is useful as scaffolds for selecting or designing a protein framework
CC with specific and favourable properties, e.g. for binding any antigen of
CC interest, or for destroying or inactivating antibody molecules. The non-
CC antibody protein is also useful in all areas where antibodies are used,
CC e.g. research, therapeutic or diagnostic fields, and for screening novel

ALL APPL.

CC binding proteins useful in the above-mentioned fields. The present
CC proteins have thermodynamic properties superior to those of natural
CC antibodies, and can be evolved rapidly in vitro. The present proteins or
CC antibody mimics exhibit improved biophysical properties, such as
CC stability under reducing conditions and solubility at high
CC concentrations. In addition, these molecules are readily expressed and
CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic
CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
CC reticulocyte lysate system). Furthermore, these proteins are extremely
CC amenable to affinity maturation techniques involving multiple cycles of
CC selection, e.g. in vitro selection using RNA-protein fusion technology,
CC phage display or yeast display systems. The present sequence is used in
CC the exemplification of the present invention

XX Sequence 94 AA;

Query Match 100.0%; Score 494; DB 5; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.2e-49;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSDVPRDLVVAATPTSLISWNRSGLQSYRYRITYGETGNSPVQEFVPPWASITATIS 60
Db |||||

QY 1 VSDVPRDLVVAATPTSLISWNRSGLQSYRYRITYGETGNSPVQEFVPPWASITATIS 60
Db |||||

QY 61 GLKPGVDYITTVAVTDKSDTYKYDDPISINVRT 94
Db |||||

QY 61 GLKPGVDYITTVAVTDKSDTYKYDDPISINVRT 94
Db |||||

RESULT 2
ABB78921

ID ABB78921 standard; peptide; 94 AA.

XX

AC ABB78921;

XX

DT 30-JUL-2002 (first entry)

XX

DE Tumour necrosis factor-alpha binding amino acid sequence T14.26.

XX

KW Protein scaffold; antibody; binding protein; immunoglobulin;

XX

KW tumour necrosis factor alpha; TNF-alpha; protein framework.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200232925-A2.

XX

PD 25-APR-2002.

XX

PF 16-OCT-2001; 2001WO-US032233.

XX

PR 16-OCT-2000; 2000US-00688566.

XX

PA (PHYL-) PHYLUS INC.

XX

PI Lipovsek D, Wagner RW, Kuimelis RG;

XX

DR WPI; 2002-444238/47.

XX

PT New non-antibody proteins having an immunoglobulin fold, useful in

XX

PT research, therapeutic or diagnostic fields, particularly as scaffolds for

XX

PT designing proteins with specific properties, e.g. for binding any antigen

XX

PT of interest.

XX

PS Claim 47; Fig 25; 94pp; English.

XX

CC The present invention describes a non-antibody protein, comprising a

XX

CC domain having an immunoglobulin-like fold, derived from a reference

XX

CC protein having a mutated amino acid sequence, where the non-antibody

CC interest, or for destroying or inactivating antibody molecules. The non-
CC antibody protein is also useful in all areas where antibodies are used,
CC e.g. research, therapeutic or diagnostic fields, and for screening novel
CC binding proteins useful in the above-mentioned fields. The present
CC proteins have thermodynamic properties superior to those of natural
CC antibodies, and can be evolved rapidly in vitro. The present proteins or
CC antibody mimics exhibit improved biophysical properties, such as
CC stability under reducing conditions and solubility at high
CC concentrations. In addition, these molecules are readily expressed and
CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic
CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
CC reticulocyte lysate system). Furthermore, these proteins are extremely
CC amenable to affinity maturation techniques involving multiple cycles of
CC selection, e.g. in vitro selection using RNA-protein fusion technology,
CC phage display or yeast display systems. The present sequence is used in
CC the exemplification of the present invention

XX Sequence 94 AA;

Query Match 100.0%; Score 494; DB 5; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.2e-49;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSDVPRDLVVAATPTSLISWNRSGLQSYRYRITYGETGNSPVQEFVPPWASITATIS 60
Db |||||

QY 1 VSDVPRDLVVAATPTSLISWNRSGLQSYRYRITYGETGNSPVQEFVPPWASITATIS 60
Db |||||

QY 61 GLKPGVDYITTVAVTDKSDTYKYDDPISINVRT 94
Db |||||

QY 61 GLKPGVDYITTVAVTDKSDTYKYDDPISINVRT 94
Db |||||

RESULT 3
ABB78939

ID ABB78939 standard; peptide; 94 AA.

XX

AC ABB78939;

XX

DT 30-JUL-2002 (first entry)

XX

DE Tumour necrosis factor-alpha binding amino acid sequence M12.01.

XX

KW Protein scaffold; antibody; binding protein; immunoglobulin;

XX

KW tumour necrosis factor alpha; TNF-alpha; protein framework.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200232925-A2.

XX

PD 25-APR-2002.

XX

PF 16-OCT-2001; 2001WO-US032233.

XX

PR 16-OCT-2000; 2000US-00688566.

XX

PA (PHYL-) PHYLUS INC.

XX

PI Lipovsek D, Wagner RW, Kuimelis RG;

XX

DR WPI; 2002-444238/47.

XX

PT New non-antibody proteins having an immunoglobulin fold, useful in

XX

PT research, therapeutic or diagnostic fields, particularly as scaffolds for

XX

PT designing proteins with specific properties, e.g. for binding any antigen

XX

PS Claim 47; Fig 25; 94pp; English.

XX

CC The present invention describes a non-antibody protein, comprising a

XX

CC domain having an immunoglobulin-like fold, derived from a reference

XX

CC protein having a mutated amino acid sequence, where the non-antibody

CC interest, or for destroying or inactivating antibody molecules. The non-
CC antibody protein is also useful in all areas where antibodies are used,
CC e.g. research, therapeutic or diagnostic fields, and for screening novel
CC binding proteins useful in the above-mentioned fields. The present
CC proteins have thermodynamic properties superior to those of natural
CC antibodies, and can be evolved rapidly in vitro. The present proteins or
CC antibody mimics exhibit improved biophysical properties, such as
CC stability under reducing conditions and solubility at high
CC concentrations. In addition, these molecules are readily expressed and
CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic
CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
CC reticulocyte lysate system). Furthermore, these proteins are extremely
CC amenable to affinity maturation techniques involving multiple cycles of
CC selection, e.g. in vitro selection using RNA-protein fusion technology,
CC phage display or yeast display systems. The present sequence is used in
CC the exemplification of the present invention

XX Sequence 94 AA;

Query Match 100.0%; Score 494; DB 5; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.2e-49;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSDVPRDLVVAATPTSLISWNRSGLQSYRYRITYGETGNSPVQEFVPPWASITATIS 60
Db |||||

QY 1 VSDVPRDLVVAATPTSLISWNRSGLQSYRYRITYGETGNSPVQEFVPPWASITATIS 60
Db |||||

QY 61 GLKPGVDYITTVAVTDKSDTYKYDDPISINVRT 94
Db |||||

QY 61 GLKPGVDYITTVAVTDKSDTYKYDDPISINVRT 94
Db |||||

RESULT 3
ABB78939

ID ABB78939 standard; peptide; 94 AA.

XX

AC ABB78939;

XX

DT 30-JUL-2002 (first entry)

XX

DE Tumour necrosis factor-alpha binding amino acid sequence M12.01.

XX

KW Protein scaffold; antibody; binding protein; immunoglobulin;

XX

KW tumour necrosis factor alpha; TNF-alpha; protein framework.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200232925-A2.

XX

PD 25-APR-2002.

XX

PF 16-OCT-2001; 2001WO-US032233.

XX

PR 16-OCT-2000; 2000US-00688566.

XX

PA (PHYL-) PHYLUS INC.

XX

PI Lipovsek D, Wagner RW, Kuimelis RG;

XX

DR WPI; 2002-444238/47.

XX

PT New non-antibody proteins having an immunoglobulin fold, useful in

XX

PT research, therapeutic or diagnostic fields, particularly as scaffolds for

XX

PT designing proteins with specific properties, e.g. for binding any antigen

XX

PS Claim 47; Fig 25; 94pp; English.

XX

CC The present invention describes a non-antibody protein, comprising a

XX

CC domain having an immunoglobulin-like fold, derived from a reference

XX

CC protein having a mutated amino acid sequence, where the non-antibody

CC interest, or for destroying or inactivating antibody molecules. The non-
CC antibody protein is also useful in all areas where antibodies are used,
CC e.g. research, therapeutic or diagnostic fields, and for screening novel
CC binding proteins useful in the above-mentioned fields. The present
CC proteins have thermodynamic properties superior to those of natural
CC antibodies, and can be evolved rapidly in vitro. The present proteins or
CC antibody mimics exhibit improved biophysical properties, such as
CC stability under reducing conditions and solubility at high
CC concentrations. In addition, these molecules are readily expressed and
CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic
CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
CC reticulocyte lysate system). Furthermore, these proteins are extremely
CC amenable to affinity maturation techniques involving multiple cycles of
CC selection, e.g. in vitro selection using RNA-protein fusion technology,
CC phage display or yeast display systems. The present sequence is used in
CC the exemplification of the present invention

XX Sequence 94 AA;

Query Match 100.0%; Score 494; DB 5; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.2e-49;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSDVPRDLVVAATPTSLISWNRSGLQSYRYRITYGETGNSPVQEFVPPWASITATIS 60
Db |||||

QY 1 VSDVPRDLVVAATPTSLISWNRSGLQSYRYRITYGETGNSPVQEFVPPWASITATIS 60
Db |||||

QY 61 GLKPGVDYITTVAVTDKSDTYKYDDPISINVRT 94
Db |||||

QY 61 GLKPGVDYITTVAVTDKSDTYKYDDPISINVRT 94
Db |||||

RESULT 3
ABB78939

ID ABB78939 standard; peptide; 94 AA.

XX

AC ABB78939;

XX

DT 30-JUL-2002 (first entry)

XX

DE Tumour necrosis factor-alpha binding amino acid sequence M12.01.

XX

KW Protein scaffold; antibody; binding protein; immunoglobulin;

XX

KW tumour necrosis factor alpha; TNF-alpha; protein framework.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200232925-A2.

XX

PD 25-APR-2002.

XX

PF 16-OCT-2001; 2001WO-US032233.

XX

PR 16-OCT-2000; 2000US-00688566.

XX

PA (PHYL-) PHYLUS INC.

XX

PI Lipovsek D, Wagner RW, Kuimelis RG;

XX

DR WPI; 2002-444238/47.

XX

PT New non-antibody proteins having an immunoglobulin fold, useful in

XX

PT research, therapeutic or diagnostic fields, particularly as scaffolds for

XX

PT designing proteins with specific properties, e.g. for binding any antigen

XX

PS Claim 47; Fig 25; 94pp; English.

XX

CC The present invention describes a non-antibody protein, comprising a

XX

CC domain having an immunoglobulin-like fold, derived from a reference

XX

CC protein having a mutated amino acid sequence, where the non-antibody

CC interest, or for destroying or inactivating antibody molecules. The non-
CC antibody protein is also useful in all areas where antibodies are used,
CC e.g. research, therapeutic or diagnostic fields, and for screening novel
CC binding proteins useful in the above-mentioned fields. The present
CC proteins have thermodynamic properties superior to those of natural
CC antibodies, and can be evolved rapidly in vitro. The present proteins or
CC antibody mimics exhibit improved biophysical properties, such as
CC stability under reducing conditions and solubility at high
CC concentrations. In addition, these molecules are readily expressed and
CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic
CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
CC reticulocyte lysate system). Furthermore, these proteins are extremely
CC amenable to affinity maturation techniques involving multiple cycles of
CC selection, e.g. in vitro selection using RNA-protein fusion technology,
CC phage display or yeast display systems. The present sequence is used in
CC the exemplification of the present invention

XX Sequence 94 AA;

Query Match 100.0%; Score 494; DB 5; Length 94;
Best Local Similarity 100.0%; Pred. No. 1.2e-49;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSDVPRDLVVAATPTSLISWNRSGLQSYRYRITYGETGNSPVQEFVPPWASITATIS 60
Db |||||

QY 1 VSDVPRDLVVAATPTSLISWNRSGLQSYRYRITYGETGNSPVQEFVPPWASITATIS 60
Db |||||

QY 61 GLKPGVDYITTVAVTDKSDTYKYDDPISINVRT 94
Db |||||

QY 61 GLKPGVDYITTVAVTDKSDTYKYDDPISINVRT 94
Db |||||

RESULT 3
ABB78939

ID ABB78939 standard; peptide; 94 AA.

XX

AC ABB78939;

XX

DT 30-JUL-2002 (first entry)

XX

DE Tumour necrosis factor-alpha binding amino acid sequence M12.01.

XX

KW Protein scaffold; antibody; binding protein; immunoglobulin;

XX

KW tumour necrosis factor alpha; TNF-alpha; protein framework.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200232925-A2.

XX

PD 25-APR-2002.

XX

PF 16-OCT-2001; 2001WO-US032233.

XX

PR 16-OCT-2000; 2000US-00688566.

XX

PA (PHYL-) PHYLUS INC.

XX

PI Lipovsek D, Wagner RW, Kuimelis RG;

XX

DR WPI; 2002-444238/47.

XX

PT New non-antibody proteins having an immunoglobulin fold, useful in

XX

PT research, therapeutic or diagnostic fields, particularly as scaffolds for

XX

PT designing proteins with specific properties, e.g. for binding any antigen

XX

PS Claim 47; Fig 25; 94pp; English.

XX

CC The present invention describes a non-antibody protein, comprising a

CC not bound as tightly by the reference protein. The non-antibody protein
CC is useful as scaffolds for selecting or designing a protein framework
CC with specific and favourable properties, e.g. for binding any antigen of
CC interest, or for destroying or inactivating antibody molecules. The non-
CC antibody protein is also useful in all areas where antibodies are used,
CC e.g. research, therapeutic or diagnostic fields, and for screening novel
CC binding proteins useful in the above-mentioned fields. The present
CC proteins have thermodynamic properties superior to those of natural
CC antibodies, and can be evolved rapidly in vitro. The present proteins or
CC antibody mimics exhibit improved biophysical properties, such as
CC stability under reducing conditions and solubility at high
CC concentrations. In addition, these molecules are readily expressed and
CC folded in prokaryotic systems (e.g. *Escherichia coli*), in eukaryotic
CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
CC reticulocyte lysate system). Furthermore, these proteins are extremely
CC amenable to affinity maturation techniques involving multiple cycles of
CC selection, e.g. in vitro selection using RNA-protein fusion technology,
CC phage display or yeast display systems. The present sequence is used in
CC the exemplification of the present invention
XX
SQ Sequence 94 AA;

Query Match 99.0%; Score 489; DB 5; Length 94;
Best Local Similarity 97.9%; Pred. No. 4.4e-49;
Matches 92; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 VSDVPRDLEVVAATPTSLRLISWNRSLGQSRYYRITYTGCGNSPVQEFVPPWASIIATIS 60
DB 1 VSDVPRDLEVVAATPTSLRLISWNRSLGQSRYYRITYTGCGNSPVQEFVPPWASIIATIS 60
QY 61 GLKPGVDYITTVAVTDKSDTYKYDDPISINVRT 94
DB 61 GLKPGVDYITTVAVTDKSDTYKYDDPISINVRT 94

RESULT 4
ABB78919
ID ABB78919 standard; peptide; 94 AA.
XX
AC ABB78919;
DT 30-JUL-2002 (first entry)
XX Tumour necrosis factor-alpha binding amino acid sequence T14.14.
DE Protein scaffold; antibody; binding protein; immunoglobulin;
KW tumour necrosis factor alpha; TNF-alpha; protein framework.
XX Homo sapiens.
OS Synthetic.
XX WO200232925-A2.
XX 25-APR-2002.
XX 16-OCT-2001; 2001WO-US032233.
XX 16-OCT-2000; 2000US-00688566.
XX (PHYL-) PHYLUS INC.
XX Lipovsek D, Wagner RW, Kuimelis RG;
PI WPI; 2002-444238/47.
XX New non-antibody proteins having an immunoglobulin fold, useful in
XX research, therapeutic or diagnostic fields, particularly as scaffolds for
XX designing proteins with specific properties, e.g. for binding any antigen
XX of interest.
XX Claim 47; Fig 25; 94pp; English.
XX The present invention describes a non-antibody protein, comprising a

CC domain having an immunoglobulin-like fold, derived from a reference
CC protein having a mutated amino acid sequence, where the non-antibody
CC protein binds with a Kd at least as tight as 10 nM to a compound that is
CC not bound as tightly by the reference protein. The non-antibody protein
CC is useful as scaffolds for selecting or designing a protein framework
CC with specific and favourable properties, e.g. for binding any antigen of
CC interest, or for destroying or inactivating antibody molecules. The non-
CC antibody protein is also useful in all areas where antibodies are used,
CC e.g. research, therapeutic or diagnostic fields, and for screening novel
CC binding proteins useful in the above-mentioned fields. The present
CC proteins have thermodynamic properties superior to those of natural
CC antibodies, and can be evolved rapidly in vitro. The present proteins or
CC antibody mimics exhibit improved biophysical properties, such as
CC stability under reducing conditions and solubility at high
CC concentrations. In addition, these molecules are readily expressed and
CC folded in prokaryotic systems (e.g. *Escherichia coli*), in eukaryotic
CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
CC reticulocyte lysate system). Furthermore, these proteins are extremely
CC amenable to affinity maturation techniques involving multiple cycles of
CC selection, e.g. in vitro selection using RNA-protein fusion technology,
CC phage display or yeast display systems. The present sequence is used in
CC the exemplification of the present invention
XX
SQ Sequence 94 AA;

Query Match 99.0%; Score 489; DB 5; Length 94;
Best Local Similarity 98.9%; Pred. No. 4.4e-49;
Matches 93; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VSDVPRDLEVVAATPTSLRLISWNRSLGQSRYYRITYTGCGNSPVQEFVPPWASIIATIS 60
DB 1 VSDVPRDLEVVAATPTSLRLISWNRSLGQSRYYRITYTGCGNSPVQEFVPPWASIIATIS 60
QY 61 GLKPGVDYITTVAVTDKSDTYKYDDPISINVRT 94
DB 61 GLKPGVDYITTVAVTDKSDTYKYDDPISINVRT 94

RESULT 5
ABB78920
ID ABB78920 standard; peptide; 94 AA.
XX
AC ABB78920;
DT 30-JUL-2002 (first entry)
XX Tumour necrosis factor-alpha binding amino acid sequence T14.23.
DE Protein scaffold; antibody; binding protein; immunoglobulin;
KW tumour necrosis factor alpha; TNF-alpha; protein framework.
XX Homo sapiens.
OS Synthetic.
XX WO200232925-A2.
XX 25-APR-2002.
XX 16-OCT-2001; 2001WO-US032233.
XX 16-OCT-2000; 2000US-00688566.
XX (PHYL-) PHYLUS INC.
XX Lipovsek D, Wagner RW, Kuimelis RG;
PI WPI; 2002-444238/47.
XX New non-antibody proteins having an immunoglobulin fold, useful in
XX research, therapeutic or diagnostic fields, particularly as scaffolds for
XX designing proteins with specific properties, e.g. for binding any antigen
XX of interest.

PS Claim 47; Fig 25; 94pp; English.

XX The present invention describes a non-antibody protein, comprising a

CC domain having an immunoglobulin-like fold, derived from a reference

CC protein having a mutated amino acid sequence, where the non-antibody

CC protein binds with a Kd at least as tight as 10 nM to a compound that is

CC not bound as tightly by the reference protein. The non-antibody protein

CC is useful as scaffolds for selecting or designing a protein framework

CC with specific and favourable properties, e.g. for binding any antigen of

CC interest, or for destroying or inactivating antibody molecules. The non-

CC antibody protein is also useful in all areas where antibodies are used,

CC e.g. research, therapeutic or diagnostic fields, and for screening novel

CC binding proteins useful in the above-mentioned fields. The present

CC proteins have thermodynamic properties superior to those of natural

CC antibodies, and can be evolved rapidly in vitro. The present proteins or

CC antibody mimics exhibit improved biophysical properties, such as

CC stability under reducing conditions and solubility at high

CC concentrations. In addition, these molecules are readily expressed and

CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic

CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit

CC reticulocyte lysate system). Furthermore, these proteins are extremely

CC amenable to affinity maturation techniques involving multiple cycles of

CC selection, e.g. in vitro selection using RNA-protein fusion technology,

CC phase display or yeast display systems. The present sequence is used in

CC the exemplification of the present invention

XX Sequence 94 AA;

SQ Query Match 99.0%; Score 489; DB 5; Length 94;

Best Local Similarity 98.9%; Pred. No. 4.4e-49;

Matches 93; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSRLLISWNRSLQSRYYRITYTGCGNSPVQEFVPPWASITATIS 60

DB 1 VSDVPRDLEVAATPTSRLLISWNRSLQSRYYRITYTGCGNSPVQEFVPPWASITATIS 60

QY 61 GLKPGVDYITITVAVTDKSDTYKYDDPISINVRT 94

DB 61 GLKPGVDYITITVAVADKSDTYKYDDPISINVRT 94

RESULT 6

ABB78911

ID ABB78911 standard; peptide; 94 AA.

AC ABB78911;

XX 30-JUL-2002 (first entry)

XX Tumour necrosis factor-alpha binding amino acid sequence S08.02.

XX Protein scaffold; antibody; binding protein; immunoglobulin;

XX tumour necrosis factor alpha; TNF-alpha; protein framework.

XX Homo sapiens.

XX Synthetic.

XX WO200232925-A2.

XX 25-APR-2002.

XX 16-OCT-2001; 2001WO-US032233.

XX 16-OCT-2000; 2000US-00688566.

XX (PHYL-) PHYLLOS INC.

XX Lipovsek D, Wagner RW, Kuimelis RG;

XX WPI; 2002-444238/47.

XX New non-antibody proteins having an immunoglobulin fold, useful in

XX research, therapeutic or diagnostic fields, particularly as scaffolds for

PT

PT designing proteins with specific properties, e.g. for binding any antigen

PT of interest.

XX Claim 47; Fig 25; 94pp; English.

XX The present invention describes a non-antibody protein, comprising a

CC domain having an immunoglobulin-like fold, derived from a reference

CC protein having a mutated amino acid sequence, where the non-antibody

CC protein binds with a Kd at least as tight as 10 nM to a compound that is

CC not bound as tightly by the reference protein. The non-antibody protein

CC is useful as scaffolds for selecting or designing a protein framework

CC with specific and favourable properties, e.g. for binding any antigen of

CC interest, or for destroying or inactivating antibody molecules. The non-

CC antibody protein is also useful in all areas where antibodies are used,

CC e.g. research, therapeutic or diagnostic fields, and for screening novel

CC binding proteins useful in the above-mentioned fields. The present

CC proteins have thermodynamic properties superior to those of natural

CC antibodies, and can be evolved rapidly in vitro. The present proteins or

CC antibody mimics exhibit improved biophysical properties, such as

CC stability under reducing conditions and solubility at high

CC concentrations. In addition, these molecules are readily expressed and

CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic

CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit

CC reticulocyte lysate system). Furthermore, these proteins are extremely

CC amenable to affinity maturation techniques involving multiple cycles of

CC selection, e.g. in vitro selection using RNA-protein fusion technology,

CC phase display or yeast display systems. The present sequence is used in

CC the exemplification of the present invention

XX Sequence 94 AA;

SQ Query Match 98.8%; Score 488; DB 5; Length 94;

Best Local Similarity 98.9%; Pred. No. 5.8e-49;

Matches 93; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSRLLISWNRSLQSRYYRITYTGCGNSPVQEFVPPWASITATIS 60

DB 1 VSDVPRDLEVAATPTSRLLISWNRSLQSRYYRITYTGCGNSPVQEFVPPWASITATIS 60

QY 61 GLKPGVDYITITVAVTDKSDTYKYDDPISINVRT 94

DB 61 GLKPGVDYITITVAVTDKSDTYKYDDPISINVRT 94

RESULT 7

ABB78915

ID ABB78915 standard; peptide; 94 AA.

AC ABB78915;

XX 30-JUL-2002 (first entry)

XX Tumour necrosis factor-alpha binding amino acid sequence T14.12.

XX Protein scaffold; antibody; binding protein; immunoglobulin;

XX tumour necrosis factor alpha; TNF-alpha; protein framework.

XX Homo sapiens.

XX Synthetic.

XX WO200232925-A2.

XX 25-APR-2002.

XX 16-OCT-2001; 2001WO-US032233.

XX 16-OCT-2000; 2000US-00688566.

XX (PHYL-) PHYLLOS INC.

XX Lipovsek D, Wagner RW, Kuimelis RG;

XX WPI; 2002-444238/47.

XX PA (PHYL-) PHYLOS INC.
XX PI Lipovsek D, Wagner RW, Kuimelis RG;
XX DR WPI; 2002-444238/47.
XX PT New non-antibody proteins having an immunoglobulin fold, useful in
XX PT research, therapeutic or diagnostic fields, particularly as scaffolds for
XX PT designing proteins with specific properties, e.g. for binding any antigen
XX PT of interest.
XX PS Claim 47; Fig 25; 94pp; English.
XX CC The present invention describes a non-antibody protein, comprising a
XX CC domain having an immunoglobulin-like fold, derived from a reference
XX CC protein having a mutated amino acid sequence, where the non-antibody
XX CC protein binds with a Kd at least as tight as 10 nM to a compound that is
XX CC not bound as tightly by the reference protein. The non-antibody protein
XX CC is useful as scaffolds for selecting or designing a protein framework
XX CC with specific and favourable properties, e.g. for binding any antigen of
XX CC interest, or for destroying or inactivating antibody molecules. The non-
XX CC antibody protein is also useful in all areas where antibodies are used,
XX CC e.g. research, therapeutic or diagnostic fields, and for screening novel
XX CC binding proteins useful in the above-mentioned fields. The present
XX CC invention has thermodynamic properties superior to those of natural
XX CC proteins and can be evolved rapidly in vitro. The present proteins or
XX CC antibodies mimic improved biophysical properties, such as
XX CC stability under reducing conditions and solubility at high
XX CC concentrations. In addition, these molecules are readily expressed and
XX CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic
XX CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
XX CC reticulocyte lysate system). Furthermore, these proteins are extremely
XX CC amenable to affinity maturation techniques involving multiple cycles of
XX CC selection, e.g. in vitro selection using RNA-protein fusion technology,
XX CC phage display or yeast display systems. The present sequence is used in
XX CC the exemplification of the present invention

XX SQ Sequence 94 AA;
Query Match 98.0%; Score 484; DB 5; Length 94;
Best Local Similarity 97.9%; Pred. No. 1.7e-48;
Matches 92; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVVAATPTSLISNRSGLQSRYYRITYGETGNSPVQEFVPPWASITATIS 60
DB 1 VSDVPRDLEVVAATPTSLISNRSGLQSRYYRITYGETGNGPVGQEFVPPWASITATIS 60

QY 61 GLKPGVDYITITVAVTDKSDTYKYDDPISINVRT 94
DB 61 GLKPGVDYITITVAVTDMSDTYKYDDPISINVRT 94

RESULT 10
ABB78916
ID ABB78916 standard; peptide; 94 AA.
XX AC ABB78916;
XX DT 30-JUL-2002 (first entry)
XX DE Tumour necrosis factor-alpha binding amino acid sequence T14.13.
XX KW Protein scaffold; antibody; binding protein; immunoglobulin;
XX KW tumour necrosis factor alpha; TNF-alpha; protein framework.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200232925-A2.
XX PD 25-APR-2002.
XX XX

PF 16-OCT-2001; 2001WO-US032233.
XX XX
PR 16-OCT-2000; 2000US-00688566.
XX XX
PA (PHYL-) PHYLOS INC.
XX XX
PI Lipovsek D, Wagner RW, Kuimelis RG;
XX XX
DR WPI; 2002-444238/47.
XX XX
PT New non-antibody proteins having an immunoglobulin fold, useful in
XX PT research, therapeutic or diagnostic fields, particularly as scaffolds for
XX PT designing proteins with specific properties, e.g. for binding any antigen
XX PT of interest.
XX PS Claim 47; Fig 25; 94pp; English.
XX CC The present invention describes a non-antibody protein, comprising a
XX CC domain having an immunoglobulin-like fold, derived from a reference
XX CC protein having a mutated amino acid sequence, where the non-antibody
XX CC protein binds with a Kd at least as tight as 10 nM to a compound that is
XX CC not bound as tightly by the reference protein. The non-antibody protein
XX CC is useful as scaffolds for selecting or designing a protein framework
XX CC with specific and favourable properties, e.g. for binding any antigen of
XX CC interest, or for destroying or inactivating antibody molecules. The non-
XX CC antibody protein is also useful in all areas where antibodies are used,
XX CC e.g. research, therapeutic or diagnostic fields, and for screening novel
XX CC binding proteins useful in the above-mentioned fields. The present
XX CC invention has thermodynamic properties superior to those of natural
XX CC proteins and can be evolved rapidly in vitro. The present proteins or
XX CC antibodies mimic improved biophysical properties, such as
XX CC stability under reducing conditions and solubility at high
XX CC concentrations. In addition, these molecules are readily expressed and
XX CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic
XX CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
XX CC reticulocyte lysate system). Furthermore, these proteins are extremely
XX CC amenable to affinity maturation techniques involving multiple cycles of
XX CC selection, e.g. in vitro selection using RNA-protein fusion technology,
XX CC phage display or yeast display systems. The present sequence is used in
XX CC the exemplification of the present invention

XX SQ Sequence 94 AA;
Query Match 97.8%; Score 483; DB 5; Length 94;
Best Local Similarity 97.9%; Pred. No. 2.2e-48;
Matches 92; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVVAATPTSLISNRSGLQSRYYRITYGETGNSPVQEFVPPWASITATIS 60
DB 1 VSDVPRDLEVVAATPTSLISNRSGLQSRYYRITYGETGNSPVQEFVPPWASITATIS 60

QY 61 GLKPGVDYITITVAVTDKSDTYKYDDPISINVRT 94
DB 61 GLKPGVDYITITVAVTDKSDTYKYDDPISINVRT 94

RESULT 11
ABB78918
ID ABB78918 standard; peptide; 94 AA.
XX AC ABB78918;
XX DT 30-JUL-2002 (first entry)
XX DE Tumour necrosis factor-alpha binding amino acid sequence T14.05.
XX KW Protein scaffold; antibody; binding protein; immunoglobulin;
XX KW tumour necrosis factor alpha; TNF-alpha; protein framework.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200232925-A2.
XX PD 25-APR-2002.
XX XX

```

XX PD 25-APR-2002.
XX PN
XX PF 16-OCT-2001; 2001WO-US032233.
XX PR 16-OCT-2000; 2000US-00688566.
XX PA (PHYL-) PHYLOS INC.
XX PI Lipovsek D, Wagner RW, Kuimelis RG;
XX DR WPI; 2002-444238/47.
XX
XX New non-antibody proteins having an immunoglobulin fold, useful in
XX research, therapeutic or diagnostic fields, particularly as scaffolds for
XX designing proteins with specific properties, e.g. for binding any antigen
XX of interest.
XX
XX Claim 47; Fig 25; 94pp; English.
XX
XX The present invention describes a non-antibody protein, comprising a
XX domain having an immunoglobulin-like fold, derived from a reference
XX protein having a mutated amino acid sequence, where the non-antibody
XX protein binds with a Kd at least as tight as 10 nM to a compound that is
XX not bound as tightly by the reference protein. The non-antibody protein
XX is useful as scaffolds for selecting or designing a protein framework
XX with specific and favourable properties, e.g. for binding any antigen of
XX interest, or for destroying or inactivating antibody molecules. The non-
XX antibody protein is also useful in all areas where antibodies are used,
XX e.g. research, therapeutic or diagnostic fields, and for screening novel
XX binding proteins useful in the above-mentioned fields. The present
XX invention has thermodynamic properties superior to those of natural
XX antibodies, and can be evolved rapidly in vitro. The present proteins or
XX antibody mimics exhibit improved biophysical properties, such as
XX stability under reducing conditions and solubility at high
XX concentrations. In addition, these molecules are readily expressed and
XX folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic
XX systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
XX reticulocyte lysate system). Furthermore, these proteins are extremely
XX amenable to affinity maturation techniques involving multiple cycles of
XX selection, e.g. in vitro selection using RNA-protein fusion technology,
XX phage display or yeast display systems. The present sequence is used in
XX the exemplification of the present invention
XX
XX Sequence 94 AA;
XX
XX Query Match 97.8%; Score 483; DB 5; Length 94;
XX Best Local Similarity 97.9%; Pred. No. 2.2e-48;
XX Matches 92; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 VSDVPRDLEVVAAATPTSRLLSNRSGLOSRYYRITYTGETGNSPVQEFVTPPWASITATIS 60
XX DB 1 VSDVPRDLEVVAAATPTSRLLSNRSGLOSRYYRITYTGETGNSPVQEFVTPPWASITATIS 60
XX
XX QY 61 GLKPGVDYTIITVAVTDKSDTYKYDDPISINRYT 94
XX DB 61 GLKPGVDYTIITVAVTDKSDTYKYDDPISINRYT 94
XX
XX RESULT 12
XX ABB78899
XX ID ABB78899 standard; peptide; 94 AA.
XX AC ABB78899;
XX DT 30-JUL-2002 (first entry)
XX
XX Tumour necrosis factor-alpha binding amino acid sequence T10.17.
XX
XX Protein scaffold; antibody; binding protein; immunoglobulin;
XX tumour necrosis factor alpha; TNF-alpha; protein framework.
XX
XX Homo sapiens.
XX

```

```

OS Synthetic.
XX WO200232925-A2.
XX PD 25-APR-2002.
XX PF 16-OCT-2001; 2001WO-US032233.
XX PR 16-OCT-2000; 2000US-00688566.
XX PA (PHYL-) PHYLOS INC.
XX PI Lipovsek D, Wagner RW, Kuimelis RG;
XX DR WPI; 2002-444238/47.
XX
XX New non-antibody proteins having an immunoglobulin fold, useful in
XX research, therapeutic or diagnostic fields, particularly as scaffolds for
XX designing proteins with specific properties, e.g. for binding any antigen
XX of interest.
XX
XX Claim 47; Fig 25; 94pp; English.
XX
XX The present invention describes a non-antibody protein, comprising a
XX domain having an immunoglobulin-like fold, derived from a reference
XX protein having a mutated amino acid sequence, where the non-antibody
XX protein binds with a Kd at least as tight as 10 nM to a compound that is
XX not bound as tightly by the reference protein. The non-antibody protein
XX is useful as scaffolds for selecting or designing a protein framework
XX with specific and favourable properties, e.g. for binding any antigen of
XX interest, or for destroying or inactivating antibody molecules. The non-
XX antibody protein is also useful in all areas where antibodies are used,
XX e.g. research, therapeutic or diagnostic fields, and for screening novel
XX binding proteins useful in the above-mentioned fields. The present
XX invention has thermodynamic properties superior to those of natural
XX antibodies, and can be evolved rapidly in vitro. The present proteins or
XX antibody mimics exhibit improved biophysical properties, such as
XX stability under reducing conditions and solubility at high
XX concentrations. In addition, these molecules are readily expressed and
XX folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic
XX systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
XX reticulocyte lysate system). Furthermore, these proteins are extremely
XX amenable to affinity maturation techniques involving multiple cycles of
XX selection, e.g. in vitro selection using RNA-protein fusion technology,
XX phage display or yeast display systems. The present sequence is used in
XX the exemplification of the present invention
XX
XX Sequence 94 AA;
XX
XX Query Match 97.4%; Score 481; DB 5; Length 94;
XX Best Local Similarity 98.9%; Pred. No. 3.8e-48;
XX Matches 93; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 VSDVPRDLEVVAAATPTSRLLSNRSGLOSRYYRITYTGETGNSPVQEFVTPPWASITATIS 60
XX DB 1 VSDVPRDLEVVAAATPTSRLLSNRSGLOSRYYRITYTGETGNSPVQEFVTPPWASITATIS 60
XX
XX QY 61 GLKPGVDYTIITVAVTDKSDTYKYDDPISINRYT 94
XX DB 61 GLKPGVDYTIITVAVTDKSDTYKYDDPISINRYT 94
XX
XX RESULT 13
XX ABB78917
XX ID ABB78917 standard; peptide; 94 AA.
XX AC ABB78917;
XX DT 30-JUL-2002 (first entry)
XX
XX Tumour necrosis factor-alpha binding amino acid sequence T14.17.
XX
XX Protein scaffold; antibody; binding protein; immunoglobulin;

```


30-JUL-2002 (first entry)
Tumour necrosis factor-alpha binding amino acid sequence T14.20.
Protein scaffold; antibody; binding protein; immunoglobulin;
tumour necrosis factor alpha; TNF-alpha; protein framework.
Homo sapiens.
Synthetic.
WO200232925-A2.
25-APR-2002.
16-OCT-2001; 2001WO-US032233.
16-OCT-2000; 2000US-00688566.
(PHYL-) PHYLLOS INC.
Lipovsek D, Wagner RW, Kuimelis RG;
WPI; 2002-444238/47.
New non-antibody proteins having an immunoglobulin fold, useful in
research, therapeutic or diagnostic fields, particularly as scaffolds for
designing proteins with specific properties, e.g. for binding any antigen
of interest.
Claim 47; Fig 25; 94pp; English.
The present invention describes a non-antibody protein, comprising a
domain having an immunoglobulin-like fold, derived from a reference
protein having a mutated amino acid sequence, where the non-antibody
protein binds with a Kd at least as tight as 10 nM to a compound that is
not bound as tightly by the reference protein. The non-antibody protein
is useful as scaffolds for selecting or designing a protein framework
with specific and favourable properties, e.g. for binding any antigen of
interest, or for destroying or inactivating antibody molecules. The non-
antibody protein is also useful in all areas where antibodies are used,
e.g. research, therapeutic or diagnostic fields, and for screening novel
binding proteins useful in the above-mentioned fields. The present
invention has thermodynamic properties superior to those of natural
antibodies, and can be evolved rapidly in vitro. The present proteins or
antibody mimics exhibit improved biophysical properties, such as
stability under reducing conditions and solubility at high
concentrations. In addition, these molecules are readily expressed and
folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic
systems (e.g. yeast), or in vitro translation systems (e.g. rabbit
reticulocyte lysate system). Furthermore, these proteins are extremely
amenable to affinity maturation techniques involving multiple cycles of
selection, e.g. in vitro selection using RNA-protein fusion technology,
phage display or yeast display systems. The present sequence is used in
the exemplification of the present invention
Sequence 94 AA;
Query Match 90.3%; Score 446; DB 5; Length 94;
Best Local Similarity 91.5%; Pred. No. 4.8e-44;
Matches 86; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
QY 1 VSDVPRLEVVAAVPTSLISWNSGLQSVYRITYGTGNSPVQFTVPPWASIIATIS 60
DB 1 VSDVPRLEVVAAVPTSLISWNSGLQSVYRITYGTGNSPVQFTVPPWASIIATIS 60
QY 61 GLKPGVDYITITVAVTDKSTYKYDDPISINRYT 94
DB 61 GLKPGVDYITITVAVTDKSTYKYDDPISINRYT 94
Search completed: February 23, 2006, 07:43:38
Job time : 187 secs

This Page Blank (uspio)

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2006, 07:47:49 ; Search time 47 Seconds
(without alignments)
165.351 Million cell updates/sec

Title: US-09-688-566-81

Perfect score: 494

Sequence: 1 VSDVPRDLEVAATPTSLRI.....VTOKSDTYKYDDPISINVRT 94

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5 COMB.pap.*
- 2: /cgn2_6/ptodata/1/iaa/6 COMB.pap.*
- 3: /cgn2_6/ptodata/1/iaa/H COMB.pap.*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pap.*
- 5: /cgn2_6/ptodata/1/iaa/RE COMB.pap.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	361	73.1	94	1	US-08-717-169-8
2	361	73.1	94	2	US-09-638-202A-110
3	361	73.1	94	2	US-09-228-901A-8
4	361	73.1	94	2	US-09-096-749A-110
5	361	73.1	94	2	US-09-637-614-110
6	361	73.1	96	2	US-09-638-202A-112
7	361	73.1	96	2	US-09-096-749A-112
8	361	73.1	96	2	US-09-637-614-112
9	361	73.1	175	1	US-08-078-683A-34
10	361	73.1	175	2	US-08-471-970A-34
11	361	73.1	175	2	US-09-723-677B-34
12	361	73.1	256	1	US-07-959-369-1
13	361	73.1	258	1	US-07-959-369-10
14	361	73.1	274	1	US-07-959-369-12
15	361	73.1	274	1	US-08-836-854-3
16	361	73.1	274	2	US-09-366-009-25
17	361	73.1	274	2	US-08-809-156B-25
18	361	73.1	274	2	US-09-775-964-25
19	361	73.1	277	1	US-07-959-369-3
20	361	73.1	279	1	US-07-959-369-11
21	361	73.1	279	1	US-08-836-854-8
22	361	73.1	281	1	US-07-959-369-4
23	361	73.1	283	1	US-07-959-369-13
24	361	73.1	283	1	US-08-836-854-7
25	361	73.1	302	1	US-08-836-854-5
26	361	73.1	302	2	US-09-366-009-29
27	361	73.1	302	2	US-08-809-156B-29

28	361	73.1	302	2	US-09-775-964-29	Sequence 29, Appl
29	361	73.1	332	1	US-08-836-854-13	Sequence 13, Appl
30	361	73.1	341	1	US-08-836-854-14	Sequence 14, Appl
31	361	73.1	367	1	US-08-836-854-18	Sequence 18, Appl
32	361	73.1	368	1	US-08-836-854-17	Sequence 17, Appl
33	361	73.1	383	1	US-07-959-369-5	Sequence 5, Appl
34	361	73.1	385	1	US-07-959-369-14	Sequence 14, Appl
35	361	73.1	385	1	US-08-836-854-10	Sequence 10, Appl
36	361	73.1	422	1	US-08-836-854-12	Sequence 12, Appl
37	361	73.1	432	1	US-07-959-369-8	Sequence 8, Appl
38	361	73.1	432	1	US-07-959-369-9	Sequence 9, Appl
39	361	73.1	432	1	US-08-836-854-20	Sequence 20, Appl
40	361	73.1	432	1	US-09-366-009-4	Sequence 4, Appl
41	361	73.1	432	2	US-08-809-156B-4	Sequence 4, Appl
42	361	73.1	432	2	US-09-775-964-4	Sequence 4, Appl
43	361	73.1	446	1	US-08-836-854-15	Sequence 15, Appl
44	361	73.1	457	1	US-08-836-854-16	Sequence 16, Appl
45	361	73.1	457	2	US-09-366-009-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1

US-08-717-169-8

; Sequence 8, Application US/08717169

; Patent No. 5922676

; GENERAL INFORMATION:

; APPLICANT: Pasqualini, Renata

; APPLICANT: Ruoslahti, Erkki

; TITLE OF INVENTION: Methods of Inhibiting Angiogenesis and

; TITLE OF INVENTION: Ameliorating Cancer By Using Superfibronection

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Campbell & Flores LLP

; STREET: 4370 La Jolla Village Drive, Suite 700

; CITY: San Diego

; STATE: California

; COUNTRY: USA

; ZIP: 92122

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/717,169

; FILING DATE: 20-SEP-1996

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P-LJ 2017

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 94 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-08-717-169-8

Query Match 73.1%; Score 361; DB 1; Length 94;

Best Local Similarity 77.7%; Pred. No. 1.8e-35;

Matches 73; Conservative 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVAATPTSLRIISWNRSLQSYRITYTGCTGNSPVQFTPPWASIAIIS 60

Db 1 VSDVPRDLEVAATPTSLRIISWNRSLQSYRITYTGCTGNSPVQFTPPWASIAIIS 60

QY 61 GLKPGVDYITTVAVTQKSDTYKYDDPISINVRT 94
| | | | | | | | | | : | : | | | | |
Db 61 GLKPGVDYITTVAVTGRGDSPASSKRPISINVRT 94

RESULT 2

US-09-638-202A-110
; Sequence 110, Application US/09638202A
; Patent No. 6462189
; GENERAL INFORMATION:
; APPLICANT: Koleda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/638,202A
; FILING DATE: 11-Aug-2000
; PRIOR APPLICATION NUMBER: 09/096,749
; FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Viksnins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 94 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 110:

US-09-638-202A-110
Query Match 73.1%; Score 361; DB 2; Length 94;
Best Local Similarity 77.7%; Pred. No. 1.8e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISWNRSLQSRYYRITYGETGNSPVQSEFTVPPWASITATIS 60
| | | | | | | | | | : | : | | | | |
Db 1 VSDVPRDLEVAATPTSLISWNRSLQSRYYRITYGETGNSPVQSEFTVPPWASITATIS 60

QY 61 GLKPGVDYITTVAVTQKSDTYKYDDPISINVRT 94
| | | | | | | | | | : | : | | | | |
Db 61 GLKPGVDYITTVAVTGRGDSPASSKRPISINVRT 94

RESULT 3

US-09-228-901A-8
; Sequence 8, Application US/09228901A
; Patent No. 6475488
; GENERAL INFORMATION:
; APPLICANT: Pasqualini, Renata
; APPLICANT: Ruoslahti, Erkki I.
; TITLE OF INVENTION: Methods of Inhibiting Angiogenesis and

US-09-638-202A-110
Query Match 73.1%; Score 361; DB 2; Length 94;
Best Local Similarity 77.7%; Pred. No. 1.8e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISWNRSLQSRYYRITYGETGNSPVQSEFTVPPWASITATIS 60
| | | | | | | | | | : | : | | | | |
Db 1 VSDVPRDLEVAATPTSLISWNRSLQSRYYRITYGETGNSPVQSEFTVPPWASITATIS 60

QY 61 GLKPGVDYITTVAVTQKSDTYKYDDPISINVRT 94
| | | | | | | | | | : | : | | | | |
Db 61 GLKPGVDYITTVAVTGRGDSPASSKRPISINVRT 94

; TITLE OF INVENTION: Ameliorating Cancer by Using Superfibronection
; FILE REFERENCE: P-TX 3416
; CURRENT APPLICATION NUMBER: US/09/228,901A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 08/717,169
; PRIOR FILING DATE: 1996-09-20
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 94
; TYPE: PRT
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-228-901A-8

Query Match 73.1%; Score 361; DB 2; Length 94;
Best Local Similarity 77.7%; Pred. No. 1.8e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISWNRSLQSRYYRITYGETGNSPVQSEFTVPPWASITATIS 60
| | | | | | | | | | : | : | | | | |
Db 1 VSDVPRDLEVAATPTSLISWNRSLQSRYYRITYGETGNSPVQSEFTVPPWASITATIS 60

QY 61 GLKPGVDYITTVAVTQKSDTYKYDDPISINVRT 94
| | | | | | | | | | : | : | | | | |
Db 61 GLKPGVDYITTVAVTGRGDSPASSKRPISINVRT 94

RESULT 4

US-09-096-749A-110
; Sequence 110, Application US/09096749A
; Patent No. 6673901
; GENERAL INFORMATION:
; APPLICANT: Koleda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/096,749A
; FILING DATE: June 12, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Viksnins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 94 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 110:

US-09-096-749A-110
Query Match 73.1%; Score 361; DB 2; Length 94;
Best Local Similarity 77.7%; Pred. No. 1.8e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISWNRSLQSRYYRITYGETGNSPVQSEFTVPPWASITATIS 60
| | | | | | | | | | : | : | | | | |
Db 1 VSDVPRDLEVAATPTSLISWNRSLQSRYYRITYGETGNSPVQSEFTVPPWASITATIS 60

QY 61 GLKPGVDYITTVAVTQKSDTYKYDDPISINVRT 94
| | | | | | | | | | : | : | | | | |
Db 61 GLKPGVDYITTVAVTGRGDSPASSKRPISINVRT 94


```
;
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/096,749A
; FILING DATE: June 12, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Vikensins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-09-096-749A-112

Query Match 73.1%; Score 361; DB 2; Length 96;
Best Local Similarity 77.7%; Pred. No. 1.9e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISWNRSLGQSRVYRITYGETGNSPVQOEFTVPPWASATIS 60
DB 3 VSDVPRDLEVAATPTSLISWNRSLGQSRVYRITYGETGNSPVQOEFTVPPWASATIS 62
QY 61 GLKPGVDYITVYAVTDKSDTYKYDDPISINYRT 94
DB 63 GLKPGVDYITVYAVTGRGDSPASSKPKISINYRT 96

RESULT 8
US-09-637-614-112
; Sequence 112, Application US/09637614
; Patent No. 6703199
; GENERAL INFORMATION:
; APPLICANT: Koleda, Shohel
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/637,614
; FILING DATE: 11-Aug-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/096,749
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CME-062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
```

```
;
; NAME: Ann S. Vikensins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-09-637-614-112

Query Match 73.1%; Score 361; DB 2; Length 96;
Best Local Similarity 77.7%; Pred. No. 1.9e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISWNRSLGQSRVYRITYGETGNSPVQOEFTVPPWASATIS 60
DB 3 VSDVPRDLEVAATPTSLISWNRSLGQSRVYRITYGETGNSPVQOEFTVPPWASATIS 62
QY 61 GLKPGVDYITVYAVTDKSDTYKYDDPISINYRT 94
DB 63 GLKPGVDYITVYAVTGRGDSPASSKPKISINYRT 96

RESULT 9
US-08-078-683A-34
; Sequence 34, Application US/08078683A
; Patent No. 5486599
; GENERAL INFORMATION:
; APPLICANT: Saunders, Scott
; APPLICANT: Bernfield, Merton
; APPLICANT: Kato, Masato
; TITLE OF INVENTION: Construction and Use of Synthetic
; TITLE OF INVENTION: Constructs Encoding Syndecan
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/078,683A
; FILING DATE: 17-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Vincent, Matthew P.
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: CME-062
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
```

; FRAGMENT TYPE: internal
US-08-078-683A-34

Query Match 73.1%; Score 361; DB 1; Length 175;
Best Local Similarity 77.7%; Pred. No. 4.2e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAFTPTSLRLISWNRSGLQSRYYRITYTGETGNSPVQSFVPPWASIIATIS 60
Db 82 VSDVPRDLEVVAAFTPTSLRLISWNRSGLQSRYYRITYTGETGNSPVQSFVPPWASIIATIS 141

Qy 61 GLKPGVDYTTITVAVTDKSDTYKYDDPISINRYT 94
Db 142 GLKPGVDYTTITVAVTGRGDSPASSKPIISINRYT 175

RESULT 10

US-08-471-970A-34
; Sequence 34, Application US/08471970A
; Patent No. 6531295
; GENERAL INFORMATION:
; APPLICANT: Saunders, Scott
; APPLICANT: Bernfield, Merton
; APPLICANT: Kato, Masato
; TITLE OF INVENTION: Construction and Use of Synthetic
; TITLE OF INVENTION: Constructs Encoding SynDecan
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,970A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/078,683
; FILING DATE: 17-JUN-1993

ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: P-41,106
; REFERENCE/DOCKET NUMBER: CME-062DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-08-471-970A-34

Query Match 73.1%; Score 361; DB 2; Length 175;
Best Local Similarity 77.7%; Pred. No. 4.2e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAFTPTSLRLISWNRSGLQSRYYRITYTGETGNSPVQSFVPPWASIIATIS 60
Db 82 VSDVPRDLEVVAAFTPTSLRLISWNRSGLQSRYYRITYTGETGNSPVQSFVPPWASIIATIS 141

Qy 61 GLKPGVDYTTITVAVTDKSDTYKYDDPISINRYT 94
Db 142 GLKPGVDYTTITVAVTGRGDSPASSKPIISINRYT 175

RESULT 11

US-09-723-677B-34
; Sequence 34, Application US/09723677B
; Patent No. 669968
; GENERAL INFORMATION:
; APPLICANT: SAUNDERS, SCOTT
; APPLICANT: BERNFIELD, MERTON
; APPLICANT: KATO, MASATO
; TITLE OF INVENTION: CONSTRUCTION AND USE OF SYNTHETIC CONSTRUCTS ENCODING SYNDECAN
; FILE REFERENCE: 101353-151
; CURRENT APPLICATION NUMBER: US/09/723,677B
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 08/471,970
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/078,683
; PRIOR FILING DATE: 1993-06-17
; PRIOR APPLICATION NUMBER: 07/856,869
; PRIOR FILING DATE: 1992-03-24
; PRIOR APPLICATION NUMBER: 07/757,654
; PRIOR FILING DATE: 1991-09-06
; PRIOR APPLICATION NUMBER: 07/746,797
; PRIOR FILING DATE: 1991-08-12
; PRIOR APPLICATION NUMBER: 07/331,585
; PRIOR FILING DATE: 1989-03-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 175
; TYPE: PRT
; ORGANISM: MUS SP;HOMO SAPIEN

US-09-723-677B-34

Query Match 73.1%; Score 361; DB 2; Length 175;
Best Local Similarity 77.7%; Pred. No. 4.2e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAFTPTSLRLISWNRSGLQSRYYRITYTGETGNSPVQSFVPPWASIIATIS 60
Db 82 VSDVPRDLEVVAAFTPTSLRLISWNRSGLQSRYYRITYTGETGNSPVQSFVPPWASIIATIS 141

Qy 61 GLKPGVDYTTITVAVTDKSDTYKYDDPISINRYT 94
Db 142 GLKPGVDYTTITVAVTGRGDSPASSKPIISINRYT 175

RESULT 12

US-07-959-369-1
; Sequence 1, Application US/07959369
; Patent No. 5302701
; GENERAL INFORMATION:
; APPLICANT: Hidetaka HASHI et al.
; TITLE OF INVENTION: No. 5302701el Functional Polypeptide
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/959,369
; FILING DATE: 19921013
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:

;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warren M. Cheek, Jr.
;; REGISTRATION NUMBER: 33,367
;; REFERENCE/DOCKET NUMBER:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-8850
;; TELEFAX:
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 256 amino acids
;; TYPE: AMINO ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: polypeptide
;; HYPOTHETICAL:
;; ANTI-SENSE:
;; FRAGMENT TYPE:
;; ORIGINAL SOURCE:
;; ORGANISM:
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; DEVELOPMENTAL STAGE:
;; HAPLOTYPE:
;; TISSUE TYPE:
;; CELL TYPE:
;; ORGANELLE:
;; IMMEDIATE SOURCE:
;; LIBRARY:
;; CLONE:
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT:
;; MAP POSITION:
;; UNITS:
;; FEATURE:
;; NAME/KEY:
;; LOCATION:
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION:
;; PUBLICATION INFORMATION:
;; AUTHORS:
;; TITLE:
;; JOURNAL:
;; VOLUME:
;; ISSUE:
;; PAGES:
;; DATE:
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO:

US-07-959-369-1
Query Match 73.1%; Score 361; DB 1; Length 256;
Best Local Similarity 77.7%; Pred. No. 6.9e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;
QY 1 VSDVPRDLEVAATPTSLRLISWNRSLQSRYYRITYGETGNSPVQBFVTPPWASIAIIS 60
Db 157 VSDVPRDLEVAATPTSLRLISWNRSLQSRYYRITYGETGNSPVQBFVTPPWASIAIIS 216
QY 61 GLKPGVDYITVYAVTDKSDTYKYDDPISINRYT 94
Db 217 GLKPGVDYITVYAVTGRGDSPASSKXPISINRYT 250

RESULT 13
US-07-959-369-10
; Sequence 10, Application US/07959369
; Patent No. 5302701
; GENERAL INFORMATION:

;; APPLICANT: Hidetaka HASHI et al.
;; TITLE OF INVENTION: No. 5302701el Functional Polypeptide
;; NUMBER OF SEQUENCES: 23
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Wenderoth, Lind & Ponack
;; STREET: 805 Fifteenth Street, N.W., #700
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: U.S.A.
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: MS-DOS
;; SOFTWARE: Wordperfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/959,369
;; FILING DATE: 19921013
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warren M. Cheek, Jr.
;; REGISTRATION NUMBER: 33,367
;; REFERENCE/DOCKET NUMBER:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 202-371-8850
;; TELEFAX:
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 258 amino acids
;; TYPE: AMINO ACID
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: polypeptide
;; HYPOTHETICAL:
;; ANTI-SENSE:
;; FRAGMENT TYPE:
;; ORIGINAL SOURCE:
;; ORGANISM:
;; STRAIN:
;; INDIVIDUAL ISOLATE:
;; DEVELOPMENTAL STAGE:
;; HAPLOTYPE:
;; TISSUE TYPE:
;; CELL TYPE:
;; CELL LINE:
;; ORGANELLE:
;; IMMEDIATE SOURCE:
;; LIBRARY:
;; CLONE:
;; POSITION IN GENOME:
;; CHROMOSOME/SEGMENT:
;; MAP POSITION:
;; UNITS:
;; FEATURE:
;; NAME/KEY:
;; LOCATION:
;; IDENTIFICATION METHOD:
;; OTHER INFORMATION:
;; PUBLICATION INFORMATION:
;; AUTHORS:
;; TITLE:
;; JOURNAL:
;; VOLUME:
;; ISSUE:
;; PAGES:
;; DATE:
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:

```

; RELEVANT RESIDUES IN SEQ ID NO:
US-07-959-369-10

Query Match      73.1%; Score 361; DB 1; Length 258;
Best Local Similarity 77.7%; Pred. No. 7e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISWNRSLQSYRYRITYGETGNSPVQEFVPPWASIIATIS 60
    |||||
Db 157 VSDVPRDLEVAATPTSLISWAPAVTVYRYRITYGETGNSPVQEFVPGSKSTATIS 216
    |||||

QY 61 GLKPGVDYITTVYAVTDKSDTYKYDDPISINRYT 94
    |||||
Db 217 GLKPGVDYITTVYAVTGRGSDPASSKPIISINRYT 250
    |||||

RESULT 14
US-07-959-369-12
; Sequence 12, Application US/07959369
; Patent No. 5302701
; GENERAL INFORMATION:
; APPLICANT: Hidetaka HASHI et al.
; TITLE OF INVENTION: No. 5302701el Functional Polypeptide
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/959,369
; FILING DATE: 19921013
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:

; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-07-959-369-12

Query Match      73.1%; Score 361; DB 1; Length 274;
Best Local Similarity 77.7%; Pred. No. 7.6e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISWNRSLQSYRYRITYGETGNSPVQEFVPPWASIIATIS 60
    |||||
Db 178 VSDVPRDLEVAATPTSLISWAPAVTVYRYRITYGETGNSPVQEFVPGSKSTATIS 237
    |||||

QY 61 GLKPGVDYITTVYAVTDKSDTYKYDDPISINRYT 94
    |||||
Db 238 GLKPGVDYITTVYAVTGRGSDPASSKPIISINRYT 271
    |||||

RESULT 15
US-08-836-854-3
; Sequence 3, Application US/08836854
; Patent No. 5824547
; GENERAL INFORMATION:
; APPLICANT: HASHINO, Kimikazu
; APPLICANT: MATSUSHITA, Hideyuki
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: METHOD OF PRODUCTION OF TRANSFECTED CELLS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,854
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/02425
; FILING DATE: 29-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 317721/1994
; FILING DATE: 29-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: HASHINO=1

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-836-854-3

Query Match 73.1%; Score 361; DB 1; Length 274;
Best Local Similarity 77.7%; Pred. No. 7.6e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;
QY 1 VSDVPRDLEVVAATPTSRLLISWNRSGLSQRYRITYGETGNSPVQBFVPPWASITATIS 60
Db 178 VSDVPRDLEVVAATPTSRLLISWDAVTVRYRITYGETGNSPVQBFVPGSKSTATIS 237
QY 61 GLKPGVDYITIVYAVTDKSDTYKYDDPISINYRT 94
Db 238 GLKPGVDYITIVYAVTGRGDSPASSKPISINYRT 271

Search completed: February 23, 2006, 07:49:09
Job time : 47 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2006, 07:59:05 ; Search time 165 Seconds
(without alignments)
238.036 Million cell updates/sec

Title: US-09-688-566-81

Perfect score: 494

Sequence: 1 VSDVPRDLVVAATPTSRLLI.....VTDKSDTYKYDDPISINVRT 94

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA_Main:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
 - 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
 - 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
 - 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
 - 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
 - 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	367.5	74.4	96	4	US-10-302-456-1
2	361	73.1	94	3	US-09-096-749A-110
3	361	73.1	94	4	US-10-174-717A-110
4	361	73.1	94	4	US-10-165-155-110
5	361	73.1	94	4	US-10-190-162-110
6	361	73.1	94	5	US-10-509-055-3
7	361	73.1	96	3	US-09-096-749A-112
8	361	73.1	96	3	US-09-903-412-110
9	361	73.1	96	3	US-09-903-412-112
10	361	73.1	96	3	US-09-903-412-121
11	361	73.1	96	4	US-10-174-717A-112
12	361	73.1	96	4	US-10-165-155-112
13	361	73.1	96	4	US-10-190-162-112
14	361	73.1	96	4	US-10-006-760-2
15	361	73.1	175	5	US-10-776-989-34
16	361	73.1	184	5	US-10-895-590-2
17	361	73.1	184	5	US-10-895-590-4
18	361	73.1	184	5	US-10-895-590-6
19	361	73.1	274	3	US-09-775-964-25
20	361	73.1	274	5	US-10-486-512-1
21	361	73.1	274	5	US-10-509-055-8
22	361	73.1	302	3	US-09-775-964-29
23	361	73.1	302	5	US-10-486-512-7
24	361	73.1	302	5	US-10-509-055-13
25	361	73.1	330	4	US-10-279-733-10
26	361	73.1	367	5	US-10-486-512-8
27	361	73.1	367	5	US-10-509-055-14

28	361	73.1	368	5	US-10-486-512-9	Sequence 9, Appli
29	361	73.1	368	5	US-10-509-055-15	Sequence 15, Appl
30	361	73.1	370	5	US-10-486-512-10	Sequence 10, Appl
31	361	73.1	370	5	US-10-509-055-16	Sequence 16, Appl
32	361	73.1	432	3	US-09-775-964-4	Sequence 4, Appli
33	361	73.1	432	3	US-09-775-964-5	Sequence 5, Appli
34	361	73.1	457	3	US-09-775-964-22	Sequence 22, Appl
35	361	73.1	457	3	US-10-486-512-11	Sequence 11, Appl
36	361	73.1	457	5	US-10-509-055-17	Sequence 17, Appl
37	361	73.1	459	5	US-10-509-055-18	Sequence 18, Appl
38	361	73.1	464	3	US-09-775-964-7	Sequence 7, Appli
39	361	73.1	472	3	US-09-775-964-21	Sequence 21, Appl
40	361	73.1	472	5	US-10-486-512-12	Sequence 12, Appl
41	361	73.1	489	3	US-09-775-964-8	Sequence 8, Appli
42	361	73.1	489	3	US-09-775-964-23	Sequence 23, Appl
43	361	73.1	549	5	US-10-486-512-5	Sequence 5, Appli
44	361	73.1	549	5	US-10-509-055-11	Sequence 11, Appl
45	361	73.1	574	3	US-09-775-964-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-10-302-456-1
; Sequence 1, Application US/10302456
; Publication No. US20030100004A1
; GENERAL INFORMATION:
; APPLICANT: Kurz, Markus
; TITLE OF INVENTION: Solid Phase Immobilization of Proteins
; TITLE OF INVENTION: and Peptides
; FILE REFERENCE: 50036/051002
; CURRENT APPLICATION NUMBER: US/10/302,456
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/333,470
; PRIOR FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-302-456-1

Query Match 74.4%; Score 367.5; DB 4; Length 96;
Best Local Similarity 80.0%; Pred. No. 5.8e-34;
Matches 76; Conservative 3; Mismatches 15; Indels 1; Gaps 1;

Qy	1	VSDVPRDLVVAATPTSRLLISWNRSGLQSRYYRITYTGCTGNSPVQSFVPPWASIATIS 60
Db	2	VSDVPRDLVVAATPTSRLLISWNRSGLQSRYYRITYTGCTGNSPVQSFVQFTVPPWASIATIS 61
Qy	61	GLKPGVDYTTTVAVTDKSDT-YKYDDPISINVRT 94
Db	62	GLKPGVDYTTTVAVTPLRWTETEAHIPINVRT 96

RESULT 2
US-09-096-749A-110
; Sequence 110, Application US/09096749A
; Patent No. US20020019517A1
; GENERAL INFORMATION:
; APPLICANT: Koleda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA

TELEPHONE: (612) 373-6900	
TELEFAX: (612) 339-3061	
INFORMATION FOR SEQ ID NO: 112:	
SEQUENCE CHARACTERISTICS:	
LENGTH: 96 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: peptide	
HYPOTHETICAL: NO	
ANTI-SENSE: NO	
FRAGMENT TYPE: internal	
ORIGINAL SOURCE:	
US-09-096-749A-112	
Query Match	73.1%; Score 361; DB 3; Length 96;
Best Local Similarity	77.7%; Pred. No. 3.2e-33;
Matches	73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;
QY	1 VSDVPRDLVVAATPTSLISWNRSGLOSRYRITYGETGNSPVQFTVPPWASIIATIS 60
Db	3 VSDVPRDLVVAATPTSLISWNRSGLOSRYRITYGETGNSPVQFTVPPWASIIATIS 62
QY	61 GLKPGVDYITIVYAVTDKSDTYKYDDPISINRYT 94
Db	63 GLKPGVDYITIVYAVTGRGDSPASSKPIISINRYT 96
RESULT 8	
US-09-903-412-110	
Sequence 110, Application US/09903412	
Publication No. US20030027319A1	
GENERAL INFORMATION:	
APPLICANT: Koide, Shohei	
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES	
FILE REFERENCE: 109.050US1	
CURRENT APPLICATION NUMBER: US/09/903,412	
CURRENT FILING DATE: 2001-07-11	
PRIOR APPLICATION NUMBER: US/09/903,412	
PRIOR FILING DATE: 2001-07-11	
NUMBER OF SEQ ID NOS: 121	
SOFTWARE: FastSeq for Windows Version 4.0	
SEQ ID NO 110	
LENGTH: 96	
TYPE: PRT	
ORGANISM: Artificial Sequence	
FEATURE:	
OTHER INFORMATION: The synthetic Fn3 gene.	
US-09-903-412-110	
Query Match	73.1%; Score 361; DB 3; Length 96;
Best Local Similarity	77.7%; Pred. No. 3.2e-33;
Matches	73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;
QY	1 VSDVPRDLVVAATPTSLISWNRSGLOSRYRITYGETGNSPVQFTVPPWASIIATIS 60
Db	3 VSDVPRDLVVAATPTSLISWNRSGLOSRYRITYGETGNSPVQFTVPPWASIIATIS 62
QY	61 GLKPGVDYITIVYAVTDKSDTYKYDDPISINRYT 94
Db	63 GLKPGVDYITIVYAVTGRGDSPASSKPIISINRYT 96
RESULT 9	
US-09-903-412-112	
Sequence 112, Application US/09903412	
Publication No. US20030027319A1	
GENERAL INFORMATION:	
APPLICANT: Koide, Shohei	
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES	
FILE REFERENCE: 109.050US1	
CURRENT APPLICATION NUMBER: US/09/903,412	
CURRENT FILING DATE: 2001-07-11	
TELEPHONE: (612) 373-6900	
TELEFAX: (612) 339-3061	
INFORMATION FOR SEQ ID NO: 112:	
SEQUENCE CHARACTERISTICS:	
LENGTH: 96 amino acids	
TYPE: amino acid	
STRANDEDNESS: single	
TOPOLOGY: linear	
MOLECULE TYPE: peptide	
HYPOTHETICAL: NO	
ANTI-SENSE: NO	
FRAGMENT TYPE: internal	
ORIGINAL SOURCE:	
US-09-096-749A-112	
Query Match	73.1%; Score 361; DB 3; Length 96;
Best Local Similarity	77.7%; Pred. No. 3.2e-33;
Matches	73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;
QY	1 VSDVPRDLVVAATPTSLISWNRSGLOSRYRITYGETGNSPVQFTVPPWASIIATIS 60
Db	3 VSDVPRDLVVAATPTSLISWNRSGLOSRYRITYGETGNSPVQFTVPPWASIIATIS 62
QY	61 GLKPGVDYITIVYAVTDKSDTYKYDDPISINRYT 94
Db	63 GLKPGVDYITIVYAVTGRGDSPASSKPIISINRYT 96
RESULT 10	
US-09-903-412-121	
Sequence 121, Application US/09903412	
Publication No. US20030027319A1	
GENERAL INFORMATION:	
APPLICANT: Koide, Shohei	
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES	
FILE REFERENCE: 109.050US1	
CURRENT APPLICATION NUMBER: US/09/903,412	
CURRENT FILING DATE: 2001-07-11	
PRIOR APPLICATION NUMBER: US/09/903,412	
PRIOR FILING DATE: 2001-07-11	
NUMBER OF SEQ ID NOS: 121	
SOFTWARE: FastSeq for Windows Version 4.0	
SEQ ID NO 121	
LENGTH: 96	
TYPE: PRT	
ORGANISM: Homo sapiens	
FEATURE:	
OTHER INFORMATION: The synthetic Fn3 gene.	
US-09-903-412-121	
Query Match	73.1%; Score 361; DB 3; Length 96;
Best Local Similarity	77.7%; Pred. No. 3.2e-33;
Matches	73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;
QY	1 VSDVPRDLVVAATPTSLISWNRSGLOSRYRITYGETGNSPVQFTVPPWASIIATIS 60
Db	3 VSDVPRDLVVAATPTSLISWNRSGLOSRYRITYGETGNSPVQFTVPPWASIIATIS 62
QY	61 GLKPGVDYITIVYAVTDKSDTYKYDDPISINRYT 94
Db	63 GLKPGVDYITIVYAVTGRGDSPASSKPIISINRYT 96
RESULT 11	
US-10-174-717A-112	
Sequence 112, Application US/10174717A	
Publication No. US20030108948A1	
APPLICANT: Koide, Shohei	
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES	
NUMBER OF SEQUENCES: 118	
CORRESPONDENCE ADDRESS:	
ADDRESS: Schwegman, Lundberg, Woessner & Kluth P.A.	
STREET: 121 South Eighth Street, St. 1600	
CITY: Minneapolis	
STATE: MN	
COUNTRY: USA	
ZIP: 55402	
COMPUTER READABLE FORM:	

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: WINDOWS
SOFTWARE: FastSEQ Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/174,717A
FILING DATE: 18-Jun-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/096,749
FILING DATE: June 12, 1998
APPLICATION NUMBER: 60/049,410
FILING DATE: June 12, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ann S. Vikens
REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 109.034US4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 373-6900
TELEFAX: (612) 339-3061
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-174-717A-112

Query Match 73.1%; Score 361; DB 4; Length 96;
Best Local Similarity 77.7%; Pred. No. 3.2e-33;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAPTSLRLISWNRSGLSQRYRITYTGTCGNSPVQEFVPPWASIIATIS 60
Db 3 VSDVPRDLEVVAAPTSLRLISWNPATVTVYRITYTGTCGNSPVQEFVPPWASIIATIS 62

Qy 61 GLKPGVDYTTITVAVTDKSDTYKYDDPISINRYT 94
Db 63 GLKPGVDYTTITVAVTGRGDSPASSKPSINRYT 96

RESULT 12
US-10-165-155-112
Sequence 112, Application US/10165155
Publication No. US20030134386A1
GENERAL INFORMATION:
APPLICANT: Koieda, Shohei
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
STREET: 121 South Eighth Street, Ste. 1600
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/165,155
FILING DATE: 06-Jun-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/096,749
FILING DATE: June 12, 1998
ATTORNEY/AGENT INFORMATION:

NAME: Ann S. Vikens
REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 109.034US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 373-6900
TELEFAX: (612) 339-3061
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-165-155-112

Query Match 73.1%; Score 361; DB 4; Length 96;
Best Local Similarity 77.7%; Pred. No. 3.2e-33;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAPTSLRLISWNRSGLSQRYRITYTGTCGNSPVQEFVPPWASIIATIS 60
Db 3 VSDVPRDLEVVAAPTSLRLISWNPATVTVYRITYTGTCGNSPVQEFVPPWASIIATIS 62

Qy 61 GLKPGVDYTTITVAVTDKSDTYKYDDPISINRYT 94
Db 63 GLKPGVDYTTITVAVTGRGDSPASSKPSINRYT 96

RESULT 13
US-10-190-162-112
Sequence 112, Application US/10190162
Publication No. US20030170753A1
GENERAL INFORMATION:
APPLICANT: Koieda, Shohei
TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
NUMBER OF SEQUENCES: 118
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
STREET: 121 South Eighth Street, Ste. 1600
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/190,162
FILING DATE: 03-Jul-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/096,749
FILING DATE: June 12, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Ann S. Vikens
REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 109.034US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 373-6900
TELEFAX: (612) 339-3061
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 96 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

```
;
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-190-162-112

Query Match          73.1%; Score 361; DB 4; Length 96;
Best Local Similarity 77.7%; Pred. No. 3.2e-33;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVVAATPTSLRLISWNRSLGQSRYYRITYTGETGNSPVQEFVPPWASITATIS 60
   ||||| ||||| ||||| ||||| : ||||| ||||| ||||| ||||| |||||
Db 3 VSDVPRDLEVVAATPTSLRLISWNRSLGQSRYYRITYTGETGNSPVQEFVPPWASITATIS 62

QY 61 GLKPGVDYTIITVYAVTDKSDTYKYDDPISINYRT 94
   ||||| ||||| ||||| ||||| : ||||| ||||| ||||| |||||
Db 63 GLKPGVDYTIITVYAVTGRGDSPASSKPIISINYRT 96

RESULT 14
US-10-006-760-2
; Sequence 2, Application US/10006760
; Publication No. US20030186385A1
; GENERAL INFORMATION:
; APPLICANT: Koide, Shohei
; TITLE OF INVENTION: METHOD OF IDENTIFYING POLYPEPTIDE MONOBODIES WHICH BIND
; FILE OF INVENTION: TO TARGET PROTEINS AND USE THEREOF
; FILE REFERENCE: 176/60901
; CURRENT APPLICATION NUMBER: US/10/006,760
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/249,756
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-006-760-2

Query Match          73.1%; Score 361; DB 4; Length 96;
Best Local Similarity 77.7%; Pred. No. 3.2e-33;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVVAATPTSLRLISWNRSLGQSRYYRITYTGETGNSPVQEFVPPWASITATIS 60
   ||||| ||||| ||||| ||||| : ||||| ||||| ||||| |||||
Db 3 VSDVPRDLEVVAATPTSLRLISWNRSLGQSRYYRITYTGETGNSPVQEFVPPWASITATIS 62

QY 61 GLKPGVDYTIITVYAVTDKSDTYKYDDPISINYRT 94
   ||||| ||||| ||||| ||||| : ||||| ||||| ||||| |||||
Db 63 GLKPGVDYTIITVYAVTGRGDSPASSKPIISINYRT 96

RESULT 15
US-10-776-989-34
; Sequence 34, Application US/10776989
; Publication No. US20050075484A1
; GENERAL INFORMATION:
; APPLICANT: SAUNDERS, SCOTT
; APPLICANT: BERNFIELD, NERTON
; APPLICANT: KATO, MASATO
; TITLE OF INVENTION: CONSTRUCTION AND USE OF SYNTHETIC CONSTRUCTS ENCODING SYNDECAN
; FILE REFERENCE: 101353-232
; CURRENT APPLICATION NUMBER: US/10/776,989
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 09/723,677
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 08/471,970
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/078,683
; PRIOR FILING DATE: 1993-06-17
; PRIOR APPLICATION NUMBER: 07/856,869
```

```
;
; PRIOR FILING DATE: 1992-03-24
; PRIOR APPLICATION NUMBER: 07/757,654
; PRIOR FILING DATE: 1991-09-06
; PRIOR APPLICATION NUMBER: 07/746,797
; PRIOR FILING DATE: 1991-08-12
; PRIOR APPLICATION NUMBER: 07/331,585
; PRIOR FILING DATE: 1989-03-29
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 175
; TYPE: PRT
; ORGANISM: MUS SP;HOMO SAPIEN
US-10-776-989-34

Query Match          73.1%; Score 361; DB 5; Length 175;
Best Local Similarity 77.7%; Pred. No. 6.7e-33;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVVAATPTSLRLISWNRSLGQSRYYRITYTGETGNSPVQEFVPPWASITATIS 60
   ||||| ||||| ||||| ||||| : ||||| ||||| ||||| |||||
Db 82 VSDVPRDLEVVAATPTSLRLISWNRSLGQSRYYRITYTGETGNSPVQEFVPPWASITATIS 141

QY 61 GLKPGVDYTIITVYAVTDKSDTYKYDDPISINYRT 94
   ||||| ||||| ||||| ||||| : ||||| ||||| ||||| |||||
Db 142 GLKPGVDYTIITVYAVTGRGDSPASSKPIISINYRT 175

Search completed: February 23, 2006, 08:04:06
Job time : 166 secs
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 23, 2006, 08:01:29 ; Search time 42 Seconds
(without alignments)
33.319 Million cell updates/sec

Title: US-09-688-566-81

Perfect score: 494

Sequence: 1 VSDPRDLEVAATPTSLRI.....VTDKSDTYKYDDPISINRYT 94

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA_New:

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	361	73.1	274	7	US-11-181-091-25
2	361	73.1	302	7	US-11-181-091-29
3	361	73.1	432	7	US-11-181-091-4
4	361	73.1	457	7	US-11-181-091-5
5	361	73.1	457	7	US-11-181-091-22
6	361	73.1	464	7	US-11-181-091-7
7	361	73.1	472	7	US-11-181-091-21
8	361	73.1	489	7	US-11-181-091-8
9	361	73.1	549	7	US-11-181-091-23
10	361	73.1	574	7	US-11-181-091-24
11	361	73.1	826	7	US-11-181-091-14
12	361	73.1	847	6	US-10-995-561-634
13	361	73.1	1259	6	US-10-995-561-625
14	361	73.1	1286	6	US-10-995-561-628
15	361	73.1	1335	6	US-10-995-561-630
16	361	73.1	1341	6	US-10-995-561-621
17	361	73.1	1348	6	US-10-995-561-624
18	361	73.1	2176	7	US-11-193-561-25
19	361	73.1	2176	7	US-11-193-771-25
20	361	73.1	2176	7	US-11-193-789-25
21	361	73.1	2176	7	US-11-193-806-25
22	361	73.1	2176	7	US-11-193-857-25
23	361	73.1	2217	7	US-11-193-561-38
24	361	73.1	2217	7	US-11-193-771-38
25	361	73.1	2217	7	US-11-193-789-38

26 361 73.1 2217 7 US-11-193-806-38 Sequence 38, Appl
27 361 73.1 2217 7 US-11-193-857-38 Sequence 38, Appl
28 361 73.1 2296 6 US-10-995-561-633 Sequence 633, App
29 361 73.1 2296 7 US-11-193-561-23 Sequence 23, Appl
30 361 73.1 2296 7 US-11-193-771-23 Sequence 23, Appl
31 361 73.1 2296 7 US-11-193-789-23 Sequence 23, Appl
32 361 73.1 2296 7 US-11-193-806-23 Sequence 23, Appl
33 361 73.1 2296 7 US-11-193-857-23 Sequence 23, Appl
34 361 73.1 2330 7 US-11-193-561-21 Sequence 21, Appl
35 361 73.1 2330 7 US-11-193-771-21 Sequence 21, Appl
36 361 73.1 2330 7 US-11-193-789-21 Sequence 21, Appl
37 361 73.1 2330 7 US-11-193-806-21 Sequence 21, Appl
38 361 73.1 2330 7 US-11-193-857-21 Sequence 21, Appl
39 361 73.1 2355 6 US-10-995-561-623 Sequence 623, App
40 361 73.1 2355 6 US-10-995-561-627 Sequence 627, App
41 361 73.1 2355 7 US-11-193-561-19 Sequence 19, Appl
42 361 73.1 2355 7 US-11-193-771-19 Sequence 19, Appl
43 361 73.1 2355 7 US-11-193-789-19 Sequence 19, Appl
44 361 73.1 2355 7 US-11-193-806-19 Sequence 19, Appl
45 361 73.1 2355 7 US-11-193-857-19 Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-11-181-091-25
; Sequence 25, Application US/11181091
; Publication No. US2006030046A1
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; Uemori, Takashi
; Ueno, Takashi
; Koyama, Nobuto
; Hashino, Kimikazu
; Kato, Ikumoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; CELLS WITH RETROVIRUS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/181,091
; FILING DATE: 14-Jul-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/775,964
; FILING DATE: 20-Feb-2001
; APPLICATION NUMBER: US/09/366,009
; FILING DATE: 02-Aug-1999
; APPLICATION NUMBER: 08/809,156
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 294382/1995
; FILING DATE: 13-NOV-1995
; APPLICATION NUMBER: JP 051847/1996
; FILING DATE: 08-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 977.6507P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394

```
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 274 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-11-181-091-25

Query Match      73.1%; Score 361; DB 7; Length 274;
Best Local Similarity 77.7%; Pred. No. 4.4e-32;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISNRSLGQSRYYRITYGETGCGNSPVQEFVTPPWASITATIS 60
Db 178 VSDVPRDLEVAATPTSLISNRSLGQSRYYRITYGETGCGNSPVQEFVTPPWASITATIS 237
QY 61 GLKPGVDYTIITVYAVTDKSDTYKYDDPISINYRT 94
Db 238 GLKPGVDYTIITVYAVTGRGDSPASSKPISINYRT 271

RESULT 2
US-11-181-091-29
; Sequence 29, Application US/111810191
; Publication No. US20060030046A1
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; Uemori, Takashi
; Koyama, Nobuto
; Hashino, Kimikazu
; Kato, Ikunoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; CELLS WITH RETROVIRUS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/181,091
; FILING DATE: 14-Jul-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/775,964
; FILING DATE: 20-Feb-2001
; APPLICATION NUMBER: US/09/366,009
; FILING DATE: 02-Aug-1999
; APPLICATION NUMBER: 08/809,156
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 294382/1995
; FILING DATE: 13-NOV-1995
; APPLICATION NUMBER: JP 051847/1996
; FILING DATE: 08-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 977.6507P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8393
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 432 amino acids
;   TYPE: amino acid
```

```
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 302 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: <Unknown>
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-11-181-091-29

Query Match      73.1%; Score 361; DB 7; Length 302;
Best Local Similarity 77.7%; Pred. No. 4.9e-32;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISNRSLGQSRYYRITYGETGCGNSPVQEFVTPPWASITATIS 60
Db 178 VSDVPRDLEVAATPTSLISNRSLGQSRYYRITYGETGCGNSPVQEFVTPPWASITATIS 237
QY 61 GLKPGVDYTIITVYAVTDKSDTYKYDDPISINYRT 94
Db 238 GLKPGVDYTIITVYAVTGRGDSPASSKPISINYRT 271

RESULT 3
US-11-181-091-4
; Sequence 4, Application US/111810191
; Publication No. US20060030046A1
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; Uemori, Takashi
; Koyama, Nobuto
; Hashino, Kimikazu
; Kato, Ikunoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; CELLS WITH RETROVIRUS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/181,091
; FILING DATE: 14-Jul-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/775,964
; FILING DATE: 20-Feb-2001
; APPLICATION NUMBER: US/09/366,009
; FILING DATE: 02-Aug-1999
; APPLICATION NUMBER: 08/809,156
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 294382/1995
; FILING DATE: 13-NOV-1995
; APPLICATION NUMBER: JP 051847/1996
; FILING DATE: 08-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 977.6507P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8393
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 432 amino acids
;   TYPE: amino acid
```



```
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-11-181-091-4

Query Match      73.1%; Score 361; DB 7; Length 432;
Best Local Similarity 77.7%; Pred. No. 7.5e-32;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAATPTSLRLISWNRSGLOSRYYRITYGETGNSPVQSFVTPPPWASIIATIS 60
Db 178 VSDVPRDLEVVAAATPTSLRLISWDAVTVRYRITYGETGNSPVQSFVTPPGSKSTATIS 237
Qy 61 GLKPGVDYTTIVYAVTDKSDTYKYDDPISINYRT 94
Db 238 GLKPGVDYTTIVYAVTGRGDSPASSKPFISINYRT 271

RESULT 4
US-11-181-091-5
; Sequence 5, Application US/11181091
; Publication No. US20060030046A1
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; Uemori, Takashi
; Ueno, Takashi
; Koyama, Nobuto
; Hashino, Kimikazu
; Kato, Ikunoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; CELLS WITH RETROVIRUS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/181,091
; FILING DATE: 14-Jul-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/775,964
; FILING DATE: 20-Feb-2001
; APPLICATION NUMBER: US/09/366,009
; FILING DATE: 02-Aug-1999
; APPLICATION NUMBER: 08/809,156
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 294382/1995
; FILING DATE: 13-NOV-1995
; APPLICATION NUMBER: JP 051847/1996
; FILING DATE: 08-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 977.6507P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear

; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-11-181-091-5

Query Match      73.1%; Score 361; DB 7; Length 457;
Best Local Similarity 77.7%; Pred. No. 8e-32;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAATPTSLRLISWNRSGLOSRYYRITYGETGNSPVQSFVTPPPWASIIATIS 60
Db 178 VSDVPRDLEVVAAATPTSLRLISWDAVTVRYRITYGETGNSPVQSFVTPPGSKSTATIS 237
Qy 61 GLKPGVDYTTIVYAVTDKSDTYKYDDPISINYRT 94
Db 238 GLKPGVDYTTIVYAVTGRGDSPASSKPFISINYRT 271

RESULT 5
US-11-181-091-22
; Sequence 22, Application US/11181091
; Publication No. US20060030046A1
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; Uemori, Takashi
; Ueno, Takashi
; Koyama, Nobuto
; Hashino, Kimikazu
; Kato, Ikunoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; CELLS WITH RETROVIRUS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/181,091
; FILING DATE: 14-Jul-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/775,964
; FILING DATE: 20-Feb-2001
; APPLICATION NUMBER: US/09/366,009
; FILING DATE: 02-Aug-1999
; APPLICATION NUMBER: 08/809,156
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 294382/1995
; FILING DATE: 13-NOV-1995
; APPLICATION NUMBER: JP 051847/1996
; FILING DATE: 08-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 977.6507P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 457 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
```

US-11-181-091-22

Query Match 73.1%; Score 361; DB 7; Length 457;
Best Local Similarity 77.7%; Pred. No. 8e-32;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLVVAATPTSLISWNRSGLQSYRYRITYGETGNSPVQEFVTPPWASITATIS 60
DB 178 VSDVPRDLVVAATPTSLISWDAPAVTVRYRITYGETGNSPVQEFVTPGSKSTATIS 237
QY 61 GLKPGVDYITTVYAVTDKSDTYKYDDPISINYRT 94
DB 238 GLKPGVDYITTVYAVTCRGDSPASSKPIISINYRT 271

RESULT 6

US-11-181-091-7
; Sequence 7, Application US/11181091
; Publication No. US20060030046A1

GENERAL INFORMATION:

APPLICANT: Asada, Kiyozo
Uemori, Takashi
Ueno, Takashi
Koyama, Nobuto
Hashino, Kimikazu
Kato, Ikunoshin

TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: WEISER & ASSOCIATES

STREET: 230 South Fifteenth Street, Suite 500

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19102

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/11/181,091

FILING DATE: 14-Jul-2005

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/775,964

FILING DATE: 20-Feb-2001

APPLICATION NUMBER: US/09/366,009

FILING DATE: 02-Aug-1999

APPLICATION NUMBER: 08/809,156

FILING DATE: <Unknown>

APPLICATION NUMBER: JP 294382/1995

FILING DATE: 13-NOV-1995

APPLICATION NUMBER: JP 051847/1996

FILING DATE: 08-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Weiser, Gerard J.

REGISTRATION NUMBER: 19,763

REFERENCE/DOCKET NUMBER: 977.6507P

TELEPHONE: 215-875-8383

TELEFAX: 215-875-8394

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 464 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-11-181-091-7

Query Match

Best Local Similarity 73.1%; Score 361; DB 7; Length 464;

Mismatches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLVVAATPTSLISWNRSGLQSYRYRITYGETGNSPVQEFVTPPWASITATIS 60
DB 178 VSDVPRDLVVAATPTSLISWDAPAVTVRYRITYGETGNSPVQEFVTPGSKSTATIS 237
QY 61 GLKPGVDYITTVYAVTDKSDTYKYDDPISINYRT 94
DB 238 GLKPGVDYITTVYAVTCRGDSPASSKPIISINYRT 271

RESULT 7

US-11-181-091-21

; Sequence 21, Application US/11181091

; Publication No. US20060030046A1

GENERAL INFORMATION:

APPLICANT: Asada, Kiyozo
Uemori, Takashi
Ueno, Takashi
Koyama, Nobuto
Hashino, Kimikazu
Kato, Ikunoshin

TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
CELLS WITH RETROVIRUS

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSEE: WEISER & ASSOCIATES

STREET: 230 South Fifteenth Street, Suite 500

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19102

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/11/181,091

FILING DATE: 14-Jul-2005

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/775,964

FILING DATE: 20-Feb-2001

APPLICATION NUMBER: US/09/366,009

FILING DATE: 02-Aug-1999

APPLICATION NUMBER: 08/809,156

FILING DATE: <Unknown>

APPLICATION NUMBER: JP 294382/1995

FILING DATE: 13-NOV-1995

APPLICATION NUMBER: JP 051847/1996

FILING DATE: 08-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Weiser, Gerard J.

REGISTRATION NUMBER: 19,763

REFERENCE/DOCKET NUMBER: 977.6507P

TELEPHONE: 215-875-8383

TELEFAX: 215-875-8394

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 472 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-11-181-091-21

Query Match

Best Local Similarity 73.1%; Score 361; DB 7; Length 472;

Mismatches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Db 178 VSDVPRDLEVAATPTSLISWDAPAVTVRYRITYGTGNSPVQEFVTPGSKSTATIS 237

Qy 61 GLKPGVDYTTIVYAVTDKSDTYKYDDPISINVRT 94
| | | | | : | : | | | | |
Db 238 GLKPGVDYTTIVYAVTGRGDSPASSKFPISINVRT 271

RESULT 10

US-11-181-091-24
; Sequence 24, Application US/11181091
; Publication No. US20060030046A1
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; Uemori, Takashi
; Koyama, Nobuto
; Hashino, Kimikazu
; Kato, Ikunoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; CELLS WITH RETROVIRUS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/11/181.091
; FILING DATE: 14-Jul-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/775,964
; FILING DATE: 20-Feb-2001
; APPLICATION NUMBER: US/09/366,009
; FILING DATE: 02-Aug-1999
; APPLICATION NUMBER: 08/809,156
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 294382/1995
; FILING DATE: 13-NOV-1995
; APPLICATION NUMBER: JP 051847/1996
; FILING DATE: 08-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 977.6507P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 574 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-11-181-091-24

Query Match 73.1%; Score 361; DB 7; Length 574;
Best Local Similarity 77.7%; Pred. No. 1e-31;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVAATPTSLISWDAPAVTVRYRITYGTGNSPVQEFVTPPWSATIS 60
| | | | | : | : | | | | |
Db 178 VSDVPRDLEVAATPTSLISWDAPAVTVRYRITYGTGNSPVQEFVTPGSKSTATIS 237

Qy 61 GLKPGVDYTTIVYAVTDKSDTYKYDDPISINVRT 94
| | | | | : | : | | | | |
Db 238 GLKPGVDYTTIVYAVTGRGDSPASSKFPISINVRT 271

RESULT 11

US-11-181-091-14
; Sequence 14, Application US/11181091
; Publication No. US20060030046A1
; GENERAL INFORMATION:
; APPLICANT: Asada, Kiyozo
; Uemori, Takashi
; Koyama, Nobuto
; Hashino, Kimikazu
; Kato, Ikunoshin
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET
; CELLS WITH RETROVIRUS
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/11/181.091
; FILING DATE: 14-Jul-2005
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/775,964
; FILING DATE: 20-Feb-2001
; APPLICATION NUMBER: US/09/366,009
; FILING DATE: 02-Aug-1999
; APPLICATION NUMBER: 08/809,156
; FILING DATE: <Unknown>
; APPLICATION NUMBER: JP 294382/1995
; FILING DATE: 13-NOV-1995
; APPLICATION NUMBER: JP 051847/1996
; FILING DATE: 08-MAR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 977.6507P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 826 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-11-181-091-14

Query Match 73.1%; Score 361; DB 7; Length 826;
Best Local Similarity 77.7%; Pred. No. 1.6e-31;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVAATPTSLISWDAPAVTVRYRITYGTGNSPVQEFVTPPWSATIS 60
| | | | | : | : | | | | |
Db 181 VSDVPRDLEVAATPTSLISWDAPAVTVRYRITYGTGNSPVQEFVTPGSKSTATIS 240

Qy 61 GLKPGVDYTTIVYAVTDKSDTYKYDDPISINVRT 94
| | | | | : | : | | | | |

```
Db      241 GLKPGVDYTTTVAVTGCGDSPASSKPIISINRYT 274

RESULT 12
US-10-995-561-634
; Sequence 634, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 634
; LENGTH: 847
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-634

Query Match      73.1%; Score 361; DB 6; Length 847;
Best Local Similarity 77.7%; Pred. No. 1.6e-31;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy      1 VSDVPRDLEVVAAATPTSLRLISWNRSGLQSRYYRITYTGTGNSPVQSFVTPPPWASIIATIS 60
      |||||
Db      165 VSDVPRDLEVVAAATPTSLRLISWDAVAVTVYRITYTGTGNSPVQSFVTPPGSKSTATIS 224
      |||||

Qy      61 GLKPGVDYTTTVAVTDKSDTYKYDDPISINRYT 94
      |||||
Db      225 GLKPGVDYTTTVAVTGCGDSPASSKPIISINRYT 258
      |||||

RESULT 13
US-10-995-561-625
; Sequence 625, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 625
; LENGTH: 1259
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-625

Query Match      73.1%; Score 361; DB 6; Length 1259;
Best Local Similarity 77.7%; Pred. No. 2.6e-31;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy      1 VSDVPRDLEVVAAATPTSLRLISWNRSGLQSRYYRITYTGTGNSPVQSFVTPPPWASIIATIS 60
      |||||
Db      522 VSDVPRDLEVVAAATPTSLRLISWDAVAVTVYRITYTGTGNSPVQSFVTPPGSKSTATIS 581
      |||||

Qy      61 GLKPGVDYTTTVAVTDKSDTYKYDDPISINRYT 94
      |||||
Db      582 GLKPGVDYTTTVAVTGCGDSPASSKPIISINRYT 615
      |||||

RESULT 14
US-10-995-561-628
; Sequence 628, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 628
; LENGTH: 1286
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-995-561-628

Query Match      73.1%; Score 361; DB 6; Length 1286;
Best Local Similarity 77.7%; Pred. No. 2.6e-31;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy      1 VSDVPRDLEVVAAATPTSLRLISWNRSGLQSRYYRITYTGTGNSPVQSFVTPPPWASIIATIS 60
      |||||
Db      522 VSDVPRDLEVVAAATPTSLRLISWDAVAVTVYRITYTGTGNSPVQSFVTPPGSKSTATIS 581
      |||||

Qy      61 GLKPGVDYTTTVAVTDKSDTYKYDDPISINRYT 94
      |||||
Db      582 GLKPGVDYTTTVAVTGCGDSPASSKPIISINRYT 615
      |||||

Search completed: February 23, 2006, 08:04:54
Job time : 42 secs
```

This Page Blank (uspto)